STIC-Biotech/ChemLib

From: Sent: To: Subject: Chan, Christina

Monday, February 11, 2002 4:06 PM Davis, Minh-Tam; STIC-Biotech/ChemLib RE: Rush search request for 09/775693

Please rush. Thanks Chris

----Original Message-----

Davis, Minh-Tam

Sent:

Monday, February 11, 2002 3:34 PM

To:

Chan, Christina

Subject:

Rush search request for 09/775693

Please search in commercial database and in issued patent files:

1) SEQ ID NO:1-and-a-polypeptide encoded by SEQ ID NO:1. Please check to see any of said polypeptide is the same as SEQ ID NO:7 or 8.

Thank you.
MINH TAM DAVIS
ART UNIT 1642, ROOM 8A01, MB 8E12

305-2008



	TYPE OF SEARCH:	VENDOR/COST(where applic.)
Searcher:	NA Sequences:	STN:
Phone:	AA Sequences:	DIALOG:
Location:	Structures:	Questel/Orbit:
Date Picked Up:	Bibliographic:	DRLink:
Date Completed:	Litigation:	Lexis/Nexis:
Searcher Prep/Review:	Full text:	Sequence Sys.:
Clerical:	Patent Family:	WWW/Internet:
Online time:	Other:	Other (specify):

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SEARCH REQUEST FORM

Requestor's Name:		Serial Number:		3	_ :
Date:	Phone: .:		Art Unit:	ij.	- '.
acterms that may have a spo	atement of search topic. Describe specifical cities or relevent cities and the search topic.	y as possible the	, keywords, etc., if known. F	ed. Define any or sequences,	1777-17

STAFF USE ONLY

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PTO-1590 (9-90)

OM of: US-09-775-693-1 to: A_Geneseq_1101:*

out_format : pfs

About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.

Command line parameters:

Communic Line Parameters: -DEV=xlp
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-QC-/cgn2_1/USpr0_spool/US09775693/runat_120 GAPOP=12.000
-QC-/cgn2_1/USPr0_spool/US09775693/runat_120 GAPOP=12.000
-QC-/cgn2_1/US0PCC-1000
-

Search information block:

-WAIT -THREADS=1

patabase: A_Geneseq_1101:*
patabase sequences: 522463
patabase sequences: 74073290
patabase length: 74073290 search time (sec): 93.400000

length: 1239 US-09-775-693-1

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                                                                                                                                                                                                                                                       seq_documentation_block;
ID AAB57016 standard; protein; 442 AA.
                                                                                                                                                                                                                                                                       XX AAF1556 to AAF16505 encode the human prostate cancer associated CC proteins, called prostate cancer antigens, given in AAB56363 to AAB57302. CC proteins, called prostate cancer antigens can have neuroprotective, Cytostatic, CC proteins at immunomodulatory, muscular, and antibacterial activities, CC cardioactive, antiinfective, gynaecological and antibacterial activities cancer active cancer cancer, chromosome can be used in gene therapy approached an ancer antigen chromosome and can be used in gene therapy and prostate cancer active and can be used in gene therapy and cancer numerous other diagnostic complying the cancer and for numerous other diagnostic complying the cancer and cancer antigens may be used to treat concerning the cancer antigens and proliferative dentification, as chromosome markers, and for numerous the cancer antigens may be used to treat concerning the cancer antigens may be used to treat concerning the cancer antigens may be used to concern in the productive proliferative concerning the cancer antigens may be used to treat concerning the cancer antigens may be used to treat concerning the cancer antigens may be used to treat concerning the cancer antigens may be used to treat concerning the cancer antigens may be used to treat concerning the cancer antigens may be used to treat concerning the cancer antigens may be used to treat concerning the cancer antigens may be used to treat concerning the cancer antigens may be used to treat concerning the cancer antigens may be used to treat concerning the cancer antigens may be used to treat concerning the cancer antigens may be used to treat concerning the cancer antigens may be used to treat concerning the cancer antigens may be used to treat concerning the cancer antigens may be used to treat concerning the cancer antigens may be used to treat concerning the cancer antigens may be used to treat concerning the cancer antigens may be used to treat the cancer antigens may be used to treat the cancer antigens may be used to treat the concerning th
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; prostate cancer; prostate cancer antigen; detection; diagnosis; neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular; neuroprotective; cytostatic; cardioactive; immininfective; gynaecological; vulnerary; gastrointestinal; neural; immune; reproductive; renal; antibacterial; gene therapy; neural; immune; reproductive disorder; antibacterial; gene therapy; cardiovascular; proliferative disorder; gastrointestinal; pulmonary; cardiovascular;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-MAR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human prostate cancer antigen protein sequence SEQ ID NO:1594.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      wound; infectious disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200055174-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-MAR-2000; 2000WO-US05988.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-SEP-2000
                                                                                                                                     alignment_scores:
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alignment_block:
US-09-775-693-1 x AAB57016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         prostate cancer associated gene sequences, referred to as prostate prostate cancer associated gene sequences, and diagnosis of cancer antigens, useful for treatment, prevention, and diagnosis of cancer antigens, useful for treatment, prevention, and diagnosis of cancer antigens, useful for treatment, prevention, and diagnosis of cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rosen CA, Ruben SM;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-587513/55.
                                                                   percent similarity:
                                                                                                                                                                                                              Sequence 442 AA;
                                                                                                                                                                                                                                                                  invention.
                                                                                                                             Quality: 2123.00
                                                                                                            Ratio:
                                                                                                       99.515
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7.4e-13 7.4e-13 7.4e-13

4e-10

0e-09 3.3e-07

.9e-06 3e-06

.6e-60 .1e-187

1.7e-05 2.1e-05 2.4e-05 4.1e-05 8.9e-05 0.0001

0.0003 0.0002 0.0004 0.0004 0.0008 0.0008 0.0010 0.0017 0.0017

Page 2

851 CCCCAGCAGCACCATCCTTTACCATGCTCATTTAGACATCGAGGCCTTC 900 297 pilevalGluAsnArgPheIleGlyMetLysSerArgGlyIleTyrGluT 314 801 CATCGTGGAGAACCGCTTCATTGGAATGAAGTCCCGAGGTATCTACGAGA 850 281 PheMetTyrLeuAsnGluValAlaGlyLysHlsGlyValGlyArgIleAs 297 751 TTCATGTACCTGAACGAAGTCGCGGGCCAAGCATGGCGTGGGCCGTATTGA 800 264 ysvalThrAsnvalLysAspGlyThrThrHisGlnThrSerLeuGluLeu 280 701 AGGTGACCAACGTCAAGGATGGCACCACCACCACCAGACCTCCTTGGAGCTC 750 247 oAsnThrProAspIleLeuGluIleGluPheLysLysGlyValProValL 264 651 CAACACCCCTGACATTCTCGAGATCGAGTTCAAAAAAGGGGTCCCTGTGA 700 231 GinalaproproglyLeuTyrThrLysThrGinAspproAlaLysAlapr 247 601 CAAGCGCCTCCAGGTCTCTACACGAAGACCCAAGGACCCAAGCCCAAAGCCCC 650 214 snieuWetHisrieserTyrGluAlaGly1lebeuGluAsnProLysAsn 230 551 ACCTCATGCACATCAGCTACGAGGCTGGAATCCTGGAGAACCCCAAGAAC 600 197 sGlylleProlleProValThrProLysAsnProTrpSerMetAspGluA 214 501 CGGGATTCCCATCCCGACTCCCAAGAACCCGTGGAGCATGGATGAGA 550 181 TyrasnargeherysgiyargasnaspreumetGluTyralarysginHi 197 451 TACAACCGGTTCAAGGCCGCAATGACCTGATGGAGTACGCAAAGCAACA 500 164 erieualaProginiteLysValIlealaProTrpArgMetProgluPhe 180 401 CACTGGCCCCCAGATAAAGGTCATTGCTCCCTGGAGGATGCCTGAATTC 450 147 yAlaThrGlyLysGlyAsnAspGlnValArgPheGluLeuSerCysTyrS 164 351 CGCCACAGGAAAGGGGAACGATCAGGTCCGGTTTGAGGTCAGCTGCTACT 400 Align seg 1/1 to: AAB57016 from: 1 to: 442 97 uPheValGluGluPheIleTrpProAlaileGInSerSerAlaieuTyrG 114 151 GCACTGAAGCTTGGGGCCAAAAAGGTGTTCATTGAGGATGTCAGCAGGGA 200 81 AlabeubysteuGlyAlatystysVaibheileGluAspValserArgGl 97 101 ATCTGGCCAACATTGGCCAGAAGGAAGGACTTCGAGGAAGCCAGGAAGAAG 150 64 yrLeuAlaAsnTleGlyGlnLysGluAspPheGluGluAlaArglysLys 80 47 rSerCysIleLeuValTrpLeuLysGlucinclyTyrAspValIleAlaT 64 51 CTCGTGCATCCTCGTGTGGCTGAAGGAACAAGGCTATGACGTCATTGCCT 100

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AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon the proteins are collectively known as colon cancer antigens have cytostatic activity and can be used in the colon cancer antigens have cytostatic activity and can be used in gene diagnosis and treatment of diseases associated with inappropriate p
                                                                                         Claim 11; Page 7623-7624; 9803pp; English.
                                                                                           Nucleic acids encoding 4277 human colon cancer-associated polypeptides, useful for preventing, diagnosing and/or treating colorectal cancers -
                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_documentation_block:

D AAG75416 standard; Protein; 442 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_name: /SIDS2/gcgdata/geneseq/geneseqp/aA2001.DAT:AAG75416
                                                                                                                                                              N-PSDB; AAH34821
                                                                                                                                                                     WPI; 2001-235357/24.
                                                                                                                                                                                 Ruben SM, Barash SC, Birse CE,
                                                                                                                                                                                                          (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                       03-NOV-1999;
                                                                                                                                                                                                                                                 29-SEP-1999;
                                                                                                                                                                                                                                                            28-SEP-2000; 2000WO-US26524.
                                                                                                                                                                                                                                                                                         05-APR-2001.
                                                                                                                                                                                                                                                                                                             WO200122920-A2.
                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                 Human; colon cancer; colon cancer antigen; diagnosis; detection;
                                                                                                                                                                                                                                                                                                                                                              Human colon cancer antigen protein SEQ ID NO:6180.
                                                                                                                                                                                                                                                                                                                                                                                                03-SEP-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1201 GAATATCATCGTCTCCAGAGCAAGGTCACTGCCAAA 1236
                                                                                                                                                                                                                                                                                                                                                                                                                                  AAG75416;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                431 GluTyrHisArgLeuGlnSerLysValThrAlaLys 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1101 GTCTCTCTACAATGAGGAGCTGGTGAACCATGAACGTGCAGGGTGATTATG 1150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          397 uSerLeuTyrAsnGluGluLeuValSerWetAsnValGlnGlyAspTyrG 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1051 GTGTCCGTCCTCAAGGCCAAGGTGTACATCCTCGGCCGGGAGTCCCCACT 1100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            364 alArgHisCysIleAlaLysSerGlnGluArgValGluGlyLysValGln 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    347 eAlaGluLeuValTyrThrGlyPheTrpHisSerProGluCysGluPheV 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  951 TGCTGAGCTGGTGTATACCGGTTTACGGCCTAGCCCTGAGTGTGAATTTG 1000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             901 ACCATGGACCGGGAAGTGCGCAAAATCAAACAAGGCCTGGGCTTGAAATT 950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      314 hrProAlaGlyThrIleLeuTyrHisAlaHisLeuAspIleGluAlaPhe 330
                                                                                                                                                                                                                             990S-0163280.
                                                                                                                                                                                                                                            99US-0157137
                                                                                                                                                                              Rosen CA;
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expression. For example, N and P may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of P by expressing in a patient's genome that affect the activity of p by expressing hactive proteins or to supplement the patients own production of P. Additionally, N may be used to produce the colon cancer-associated Ps, additionally, N may be used to produce the colon cancer decided in the prevention, diagnosis by inserting the nucleic acids into a host cell and culturing the cell by inserting the proteins. N and P can be used in the prevention, diagnosis to express the proteins. N and P can be used in the prevention of the and AAB77789 represent sequences used in the exemplification of the present invention.

N.B. Pages 666 to 682 and page 7053 of the sequence listing were missing at time of publication, meaning no sequences are present for SEQ ID NO:1027 to 1052, 7921 and 7922.

88888888888888 alignment_scores: alignment_block: US-09-775-693-1 x AAG75416 percent Similarity: 99.515 Align seg 1/1 to: AAG75416 from: 1 to: 442 Sequence 442 AA; 1 ATGTCCAGCAAAGGCTCCGTGGTTCTGGCCTACAGTGGCGGCCTGGACAC 50 Quality: 2123.00 Ratio: 5.178 Percent Identity: 99.272 Length:

81 AlaLeuLysLeuGlyAlaLysLysValPheIleGluAspValSerArgGl 97

351 CGCCACAGGAAAGGGGAACGATCAGGTCCGGTTTGAGCTCAGCTGCTACT 400

> 601 CAAGCGCCTCCAGGTCTCTACACGAAGACCCAGGACCCAGGCCAAAGCCCC 650 214 snLeuMetHisIleSerTyrGluAlaGlyIleLeuGluAsnProLysAsn 230 651 CAACACCCCTGACATTCTCGAGATCGAGTTCAAAAAAAGGGGTCCCTGTGA 700 701 AGGTGACCAACGTCAAGGATGGCACCACCCACCAGACCTCCTTGGAGCTC 750 751 TTCATGTACCTGAACGAAGTCGCGGGCAAGCATGGCGTGGGCCGTATTGA 800 851 CCCCAGCAGCACCATCCTTTACCATGCTCATTTAGACATCGAGGCCTTC 900 801 CATCGTGGAGAACCGCTTCATTGGAATGAAGTCCCGAGGTATCTACGAGA 850 1051 GTGTCCGTCCTCAAGGGCCAGGTGTACATCCTCGGCCGGGAGTCCCCACT 1100 1001 TCCGCCACTGCATCGCCAAGTCCCAGGAGCGAGTGGAAGGGAAAGTGCAG 1050 331 ThrMetAspArgGluvalArgLysIleLysGlnGlyLeuGlyLeuLysPh 347 901 ACCATGGACCGGGAAGTGCGCAAAATCAAACAAGGCCTGGGCTTGAAATT 950 314 hrProAlaGlyThrileLeuTyrHisAlaHisLeuAspIleGluAlaPhe 330 951 TGCTGAGCTGGTGTATACCGGTTTTACGGCCTAGCCCTGAGTGTGAATTTG 1000 1151 AGCCAACTGATGCCACCGGGTTCATCAACATCAATTCCCTCAGGCTGAAG 1200 1101 GTCTCTCTACAATGAGGAGCTGGTGAGCATGAACGTGCAGGGTGATTATG 1150 364 alargHisCysIleAlaLysSerGinGluargValGluGlyLysValGin 380 1201 GAATATCATCGTCTCCAGAGCAAGGTCACTGCCAAA 1236 414 luProThrAspAlaThrGlyPheIleAsnIleAsnSerLeuArgLeuLys 430 eAlaGluLeuValTyrThrGlyPheTrpHisSerProGluCysGluPheV 364

seq_name: /SIDS2/gcgdata/geneseq/geneseqp/AA2001.DAT:AAG82054

seq_documentation_block: AAG82054 standard; Protein; 367 AA

AAG82054;

(first entry)

S. epidermidis open reading frame protein sequence SEQ ID NO:1202. 03-SEP-2001

Staphylococcus epidermidis SR1 strain; infection; diagnosis;

staphylococcus epidermidis vaccination; endocarditis.

WO200134809-A2.

17-MAY-2001

09-NOV-2000; 2000WO-US30782.

09-NOV-1999;

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alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ANH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides CC (II), given in AAG881454 to AAG83120, from Staphylococcus epidermidis. CC (I) and (II) can have antibacterial activity and therefore can be used containing them which are used to produce the vaccination. The nucleic acids (I) may be used to produce the containing them which are used to produce hosts cells which express the CC used to vaccinate subjects and to raise antibodies against the bacteria. CC used to vaccinate subjects and to raise antibodies against the bacteria. CC treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to CC AAH55090 represent specifically claimed S. epidermidis. Government of the prosent intention. CC CAH55098 represent oligonucleotide sequences and primers which are used CC used to the exemplification of the present invention. AAH55091 to CC N.B. The present intention specifically claims all the polynucleotide contained sequences and primers which are used CC used neces given in the sequence listing of the present specification, cc though sequences are given in the disclosure for SEQ ID No:4454 so even cc mosequences are present for SEQ ID NO:4455 to 4461.
                                                                                                                                                                                                                                                                                                                                                                                                       Align seg 1/1 to: AAG82054 from: 1 to: 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
             260 ACCTCCTGGGCACCTCTTTGCCAGGCCCTGCATCGCCCGCAAACAAGTG 309
                                                                                210 GGAGTTCATCTGGCCGGCCATCCAGTCCAGCGCACTGTATGAGGACCGCT 259
                                                                                                                                       160 CTTGGGGCCAAAAAGGTGTTCATTGAGGATGTCAGCAGGGAGTTTGTGGA 209
                                                                                                                                                                                                                        110 ACATTGGCCAGAAGGAAGACTTCGAGGAAGCCAGGAAGAAGGCACTGAAG 159
                                               68 pAspTyrValSerTyrAlaIleLysGlyAsnLeuMetTyrGluAsnAlaT 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                -09-775-693-1 x AAG82054
                                                                                                                  52 MetGlyAlavalGluCysHisileIleAspAlaThrLysGluPheSerAs 68
                                                                                                                                                                                      35 spValGlyGluGlyLysAspLeuAspValValTyrGlnLysAlaLeuAsp 51
                                                                                                                                                                                                                                                          18 aValGlnTrpLeuIleAspLysGlyTyrAspValValAlaCysCysLeuA 35
                                                                                                                                                                                                                                                                                                                           60 CCTCGTGTGGCTGAAGGAACAAGGCTATGACGTCATTGCCTATCTGGCCA 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 18; Page 345; 2188pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acids encoding polypeptides from Staphylococcus epidermidis, useful for vaccinating against infections, e.g. endocarditis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAH52904.
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Ratio:
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72.654
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Length:
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seq_documentation_block:

seq_name: /SIDS2/gcgdata/geneseq/geneseqp/AA2001.DAT:AAG91292

r,d"

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alignment_scores:
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                                                                                                                                                                                                                                                 Quality: 619.50
Ratio: 2.261
Percent Similarity: 66.344
                                                                                                                                                     Align seg 1/1 to: AAG91292 from: 1 to: 401
                                                                                                                                                                                           US-09-775-693-1 x AAG91292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C glutamicum protein fragment SEQ ID NO: 5046.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-SEP-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-DEC-1999; 99JP-0377484.
07-APR-2000; 2000JP-0159162.
03-AUG-2000; 2000JP-0280988.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Corynebacterium glutamicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         organic acid synthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Coryneform bacterium; amino acid synthesis; vitamin; saccharide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-DEC-2000; 2000EP-0127688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-JUN-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a area useful for identifying the mutation point of a gene derived from a analysing the expression profile or expression pattern of a gene derived analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing from coryneform bacterium. Coryneform bacteria are useful for producing producing from coryneform bacterian. Coryneform bacteria are useful for producing from coryneform bacterian. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a protein described in the exemplification of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nakagawa S,
Tateishi N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (KYOW ) KYOWA HAKKO KOGYO KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAH66511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 17; SEQ ID NO: 5046; 246pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                   Sequence 401 AA;
                                                                                                                                                                                                                                                                                                                                                                                                       European Patent Office.
                                     69 GCTGAAGGAACAA...GGCTATGACGTCATTGCCTATCTGGCCAACATTG 115
                                                                                                              19 GTGGTTCTGGCCTACAGTGGCGGCCTGGACACCTCGTGCATCCTCGTGTG 68
21 rLeuLysLysMetIleAspGlyGluValIleAlaValSerLeuAspLeuG 38
                                                                        5 IleValLeuAlaTyrSerGlyGlyLeuAspThrThrValAlaIleProTy 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2001-376931/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Senoh A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mizoguchi H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              H, Ando S, Hayashi M, Ochiai K, Ikeda M, Ozaki A;
                                                                                                                                                                                                                                                           Gaps: 8
Percent Identity: 35.351
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116 GCCAG...AAGGAAGACTTCGAGGAAGCCAGGAAGAAGGCACTGAAGCTT 162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                313 ATCGCCCAGCGGAGGGGGCCAAGTATGTGTCCCACGGCGCCACAGGAAA 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            263 TOCTGGGCACCTCTTGCCAGGCCCTGCATCGCCCGCAAACAAGTGGAA 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     213 GTTCATCTGGCCGGCCATCCAGTCCAGCGCACTGTATGAGGACCGCTACC 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38 lyGlnGlyGlyGluAsnMetAspAsnValArgGlnArgAlaLeuAspAla 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      105 AlaGlyLysGlnPheAsnGlyThrHisValAlaHisGlyCysThrGlyLy 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55 GlyAlaAlaGluSerTleValValAspAlaLysAspGluPheAlaGluGi 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   138 snLeuGluIleIleAlaProAlaArgAspPheAlaTrpThr......... 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           413 AGATAAAGGTCATTGCTCCC.....TGGAGGATGCCTGAA 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 sGlyAsnAspGlnValArgPheGluValGlyPheMetAspThrAspProA 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            363 GGGGAACGATCAGGTCCGGTTTGAGCTCAGCTGCTACTCACTGGCCCCCC 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           71 uTyrCysLeuproThrIleLysAlaAsnGlyMetTyrMetLysGlnTyrP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       152 .....ArgAspLysAlaIleAlaPheAlaGluGl 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      448 TTCTACAACCGGTTCAAGGGCCGCAATGACCTGATGGAGTACGCAAAGCA 497
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          178 lnAsnValTrpGlyArgAlaIleGluThrGlyTyrLeuGluAspLeuTrp 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    548 AGAACCTCATGCACATCAGCTACGAGGCTGGAATCCTGGAGAACCCCCAAG 597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   161 uAsnAsnValproIleGluGlnSerValLysSerProPheSerIleAspG 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             498 ACACGGGATTCCCCATCCCGGTCACTCCCAAGAACCCGTGGAGCATGGATG 547
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         227 alSerIle.....AspGlyArgPro...ValSerValLeuGln
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                                                                                                                                                                                                                                                                            848 AGACCCCAGCAGCACCATCCTTTACCATGCTCATTTAGACATCGAGGCC 897
                                                                                                                                                                                                                                                                                                                           798 TGACATCGTGGAGAACCGCTTCATTGGAATGAAGTCCCGAGGTATCTACG 847
                                                                                                                                                                                  898 TTCACCATGGACCGGGAAGTGCGCAAAATCAAACAAGGCCTGGGCTTGAA 947
                                                                                                                                                                                                                               272 luAlaProGlyAlaIleAlaLeuIleLysAlaHisGluAlaLeuGluAsp
998 TTGTCCGCCACTGCATCGCCAAGTCCCAGGAGCGAGTGGAAGGGAAAGTG 1047
                                            948 ATTTGCTGAGCTGCTGTATACCGGTTTACGGCCTAGCCCTGAGTGTGAAT 997
                                                                                                                                      289 ValThrIleGluArgGluLeuAlaArgTyrLysArgGlyValAspAlaAr 305
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seq_name: /SIDS2/gcgdata/geneseq/geneseqp/AA2001.DAT:AAB79801
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                                            08-JUL-1999;
09-JUL-1999;
09-JUL-1999;
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08-JUL-1999;
08-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                               04-JAN-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Corynebacterium glutamicum; metabolic pathway protein; MP protein; fine chemical production; microorganism; organic acid; nucleoside; nonproteinogenic amino acid; purine base; pyrimidine base; nucleotide; lipid; saturated fatty acid; unsaturated fatty acid; of oil; vitamin;
                                                                                                                                                                                                                                                                                                                                    01-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                25-JUN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Corynebacterium glutamicum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          carbohydrate; aromatic compound; cofactor; polyketide; enzyme.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1148 ATGAGCCAACTGATGCCACCGGGTTCATCAACATCAACTTCCCTCAGGCTG 1197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Corynebacterium glutamicum MP protein sequence SEQ ID NO:336.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB79801 standard; Protein; 401 AA.
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322 erLeuAspAlaPheIleAspSerThrGlnGluHisValThrGlyAspIle 338
                            99DE-1031634
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99DE-1032130
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21 rLeuLysLysMetIleAspGlyGluValIleAlaValSerLeuAspLeuG
                                                 69 GCTGAAGGAACAA...GGCTATGACGTCATTGCCTATCTGGCCAACATTG 115
                                                                                                                                  19 GTGGTTCTGGCCTACAGTGGCGGCCTGGACACCTCGTGCATCCTCGTGTG 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                compounds, vitamins, cofactors, polyketides and enzymes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 20; Page 656-657; 1737pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acids from Corynebacterium glutamicum encoding metabolic pathway proteins, useful for producing fine chemicals in microorganisms, including organic acids, nonproteinogenic amino acids, and purine and pyrimidine bases.
                                                                                                        5 IleValLeuAlaTyrSerGlyGlyLeuAspThrThrValAlaIleProTy 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-SEP-1999;
03-SEP-1999;
03-SEP-1999;
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14-JUL-1999;
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2.261
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99DE-1040832.
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99US-0148613.
99DE-1040764.
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99DE-1042077.
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99DE-1032229
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Gaps:
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116 GCCAG...AAGGAAGACTTCGAGGAAGCCCAGGAAGAAGGCACTGAAGCTT 162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            152 .....ArgAspLysAlaIleAlaPheAlaGluGl 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         138 snLeuGluIleIleAlaProAlaArgAspPheAlaTrpThr....... 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 413 AGATAAAGGTCATTGCTCCC.....TGGAGGATGCCTGAA 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              448 TTCTACAACCGGTTCAAGGGCCGCAATGACCTGATGGAGTACGCAAAGCA 497
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           698 TGAAGGTGACCAACGTCAAGGATGGCACCACCCACCAGACCTCCTTGGAG 747
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211 y...AsnAlaProAspGluValIleIleSerPheGluGlyGlyLysProV 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    648 CCCCAACACCCCTGACATTCTCGAGATCGAGTTCAAAAAAAGGGGTCCCTG 697
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           227 alSerIle......AspGlyArgPro...ValSerValLeuGln 238
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                                                                                                                                                                                                                                                                             848 AGACCCCAGCAGCACCATCCTTTACCATGCTCATTTAGACATCGAGGCC 897
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998 TTGTCCGCCACTGCATCGCCAAGTCCCAGGAGCGAGTGGAAGGGAAAGTG 1047
                                            305 gTrpAlaGluGluValTyrAspGlyLeuTrpPheGlyProLeuLysArgS 322
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             116 GCCAGAAG...GAAGACTTCGAGGAAGCCAGGAAGAAGGCACTGAAGCTT 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         115 pLeuLysGluAsnTyrGlyCysGluValValCysPheThrAlaAspValG 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      163 GGGGCCAAAAAGGTGTTCATTGAGGATGTCAGCAGGAGTTTGTGGAGGA 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          149 GlyAlaSerGlnLeuValValAsnAspLeuThrGluGluPheValLysAs 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               213 GTTCATCTGGCCGGCCATCCAGTCCAGCGCACTGTATGAGGACCGCTACC 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69 GCTGAAGGAACAA...GGCTATGACGTCATTGCCTATCTGGCCAACATTG 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99 ValValLeuAlaTyrSerGlyGlyLeuAspThrSerVallleValProTr 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19 GTGGTTCTGGCCTACAGTGGCGGCCTGGACACCTCGTGCATCCTCGTGTG 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                          413 AGATAAAGGTCATTGCTCCCTGGAGGATGCCTGAATTCTACAACCGGTTC 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                363 GGGGAACGATCAGGTCCGGTTTGAGCTCAGCTGCTACTCACTGGCCCCCC 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               199 ValalaalaGluvalGlyAlaAspAlaValAlaHisGlyCysThrGlyLy 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             313 ATCGCCCAGCGGGAGGGGCCAAGTATGTGTCCCACGGCGCCACAGGAAA 362
                                                                                                                                                                                                                                                                                                                                                                                                              513 CCCGGTCACTCCCAAGAACCCGTGGAGCATGGATGAGAACCTCATGCACA 562
                                                                                                                                                                                                                                                                                                                      463 AAGGGCCGCAATGACCTGATGGAGTACGCAAAGCAACACGGGATTCCCAT 512
                                                295 AspMetTyr 297
                                                                                                                                     278 euSerHisGluGlyAspLeuLeuGluAspProAlaAsnGluProLysLys 294
                                                                                                                                                                                   563 TCAGCTACGAGGCTGGAATCCTGGAGACCCCAAGAACCAAGCGCCTCCA 612
                                                                                                 613 GGTCTCTAC 621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pPheIlePheProCysLeuArgAlaGlyAlaIleTyrGluArgLysTyrL 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sGlyAsnAspGlnValArgPheGluLeuThrPhePheSerLeuAsnProG 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           euLeuGlyThrSerMetAlaArgProValIleAlaLysAlaMetValAsp 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCCTGGGCACCTCTTGCCAGGCCCTGCATCGCCCGCAAACAAGTGGAA 312
                                                                                                                                                                                                                               lProValThrLysLysSerIleTyrSerArgAspIleAsnLeuTrpHisL 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99US-0161992.
99US-0161993.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99US-0162142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      80.296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          533.00
3.270
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seq_documentation_block:

AAB53535 standard; Protein; 146 AA.

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XX
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                                                                                                                                                                                                             alignment_block:
US-09-775-693-1 x AAB53535
                                                                                                                                                                Align seg 1/1 to: AAB53535 from: 1 to: 146
                                                                                                                                                                                                                                                                         Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human colon cancer antigen protein sequence SEQ ID NO:1075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-MAR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      neural disorder; immune system disorder; muscular disorder; reproductive disorder; gastrointestinal disorder; renal disorder; infectious disease; cardiovascular disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   identification; cytostatic; cardioactive; neuroprotective; vulnerary; immunomodulatory; muscular; gynaecological; gastrointestinal; nephrotropic; antiinfective; antibacterial; gene therapy; wound;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Colon cancer associated gene sequences, referred to as colon cancer antigens, useful for the treatment, prevention, and diagnosis of colon disorders such as colon cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200055351-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       can be used in gene therapy. The colon cancer antigen polynicleotides, proteins and antibodies to the proteins are useful for the prevention, proteins and antibodies to the proteins are useful for the prevention, proteins and antibodies of colon disorders, such as colon cancer. The polynicleotides may be used in disorders, such as for polynicleotides may be used in disorders and research, such as for chromosome identification, and as hybridisation probes. The proteins chromosome identification, and as hybridisation probes. The proteins may also be used to prevent diseases such as neural disorders, immune may also be used to prevent diseases such as neural disorders, system disorders, muscular diseases, reproductive disorders gastrointestinal disorders, wounds, renal disorders, infectious diseases, and cardiovascular disorders. AAC98764 to AAC98772 and AAB54007 represent sequences used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08-MAR-2000; 2000WO-US05883.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-SEP-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAC97991 to AAC98763 encode the human colon cancer associated proteins, called human colon cancer antigens, given in AAB53234 to AAB54006. The human colon cancer antigens can have cytostatic, cardioactive, muscular; neuroprotective, immunomodulatory, gynaecological, gastrointestinal, neuroprotective, immunomodulatory, gynaecological, gastrointestinal, wilnerary, nephrotropic, antiinfective and antibacterial activities, and vulnerary, nephrotropic, antiinfective and antibacterial activities, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAC98292.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-587534/55.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rosen CA, Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 11; Page 1660-1661; 2104pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
838 GGTATCTACGAGACCCCCAGCAGGCACCATCCTTTACCATGCTCATTTAGA 887
                                                                                  colon cancer; colon cancer antigen; diagnosis; detection;
                                                                                                                                                                                                                                                                                                                 Quality:
                                                                                                                                                                                                                                                                                                  Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                      146 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99US-0124270.
                                                                                                                                                                                                                                                                              4.926
94.949
                                                                                                                                                                                                                                                                                                                        463.00
                                                                                                                                                                                                                                                                  Length: 99
Gaps: 0
Percent Identity: 92.929
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seq_documentation_block:
ID AAM16101 standard; Protein; 59 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_name:
                                                                                                          The present invention relates to human single exon nucleic acid probes (SEMP: see AAI10068-AAI28459). The present sequence is a peptide encoded by one such probe. The SEMPs are derived from human HeLa cells. The SEMPs measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably
  Sequence
                                at ftp.wipo.int/pub/published_pct_sequences.
                                            Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                Claim 27; SEQ ID No 20927; 487pp; English.
                                                                                                                                                                                                                                                                                                                                                                           Human genome-derived single exon nucleic acid probes useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-FEB-2000; 2000US-0180312.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-JAN-2001; 2001WO-US00670.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1088 GGGAGTCCCCACTGTCTCTACAATGAGGAGCTGGTGAGCATGAAC 1134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200157278-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1038 AGGGAAAGTGCAGGTGTCCGTCCTCAAGGGCCCAGGTGTACATCCTCGGCC 1087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Probe; human; microarray; gene expression; cervical epithelial cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peptide #2535 encoded by probe for measuring cervical gene expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-OCT-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cervical cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAM16101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      988 GAGTGTGAATTTGTCCGCCACTGCATCGCCAAGTCCCCAGGAGCGAGTGGA 1037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84 rgGluSerProLeuSerLeuTyrAsnGluGluLeuValSerMetAsp 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51 GluCysGluPheValArgHisCysTleAlaLysSerGlnGluArgValGl 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGGGCTTGAAATTTGCTGAGCTGGTGTATAACCGGTTTACGGCCTAGCCCT 987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /SIDS2/gcgdata/geneseq/geneseqp/AA2001.DAT:AAM16101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              :::វវាមេវិញមេវិញមេវិញមេវិញមេវិញមេវិញមេវិញ
                                                                                                                                                                                                                                                                                                                                                       gene expression in human cervical epithelial cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hanzel DK,
59 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000US-0207456
2000US-0608408
2000US-0632366
2000US-0234687
2000US-0234687
2000US-0236359
2000US-0024263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chen W, Rank DR;
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alignment_scores:

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seq_name: /SIDS2/gcgdata/geneseq/geneseqp/AA2001.DAT:AAM28592
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Align seg 1/1 to: AAM16101 from: 1 to: 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-775-693-1/rev x AAM16101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
       The present invention relates to single exon nucleic acid probes (SENP: see AAI31315-AAI57546). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of
                                                                                                   Claim 27; SEQ ID No 28861; 654pp; English.
                                                                                                                                         Human genome-derived single exon nucleic acid probes useful for
                                                                                                                                                                                 WPI; 2001-488897/53.
                                                                                                                                                                                                               Penn SG,
                                                                                                                                                                                                                                    (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                                    04-OCT-2000;
                                                                                                                                                                                                                                                                                 26-MAY 2000; 2000US-0207456
30-JUN-2000; 2000US-0608408
03-AUG-2000; 2000US-0632366
21-SEP-2000; 2000US-0234687
27-SEP-2000; 2000US-0236359
                                                                                                                                                                                                                                                                                                                                                        04-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                     30-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                  09-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200157272-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     genetic disorder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Probe; microarray; human; placenta; antenatal diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peptide #2629 encoded by probe for measuring placental gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-OCT-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAM28592;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAM28592 standard; Protein; 59 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             423 GACCTTTATCTGGGG 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             473 TTGCGGCCCTTGAACCGGTTGTAGAATTCAGGCATCCTCCAGGGAGCAAT 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     523 GAGTGACCGGGATGGGAATCCCGTGTTGCTTTGCGTACTCCATCAGGTCA 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            573 CTCGTAGCTGATGTGCATGAGGTTCTCATCCATGCTCCACGGGTTCTTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51 AspLeuAsnLeuGly 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34 leAlaAlaIleGluProValValGluLeuGlyHisProProGlySerAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17 uSerAspTrpAspGlyAsnProMetLeuLeuCysValPheHisGlnIleI 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 LeulleAlaAspThrHisGluValLeuValHisAspProArgValLeuGl 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Quality:
Ratio:
                                                                                                                                gene expression in human placenta -
                                                                                                                                                                                                          Hanzel DK,
                                                                                                                                                                                                                                                                 2000GB-0024263.
                                                                                                                                                                                                                                                                                                                                                       2000US-0180312
                                                                                                                                                                                                                                                                                                                                                                                  2001WO-US00663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90.909
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4.560
                                                                                                                                                                                                          Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Identity: 76.364
                                                                                                                                                                                                          Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50
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SS

Sequence

59 AA;

alignment_scores:

Quality:

228.00

Length:

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alignment_block:
US-09-775-693-1/rev x AAM28592
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity: 90.909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to: AAM28592 from: 1 to: 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       573 CTCGTAGCTGATGTGCATGAGGTTCTCATCCATGCTCCACGGGTTCTTGG 524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               523 GAGTGACCGGGATGGGAATCCCGTGTTGCTTTGCGTACTCCATCAGGTCA 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         473 TTGCGGCCCTTGAACCGGTTGTAGAATTCAGGCATCCTCCAGGGAGCAAT 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   423 GACCTTTATCTGGGG 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17 uSerAspTrpAspGlyAsnProMetLeuLeuCysValPheHisGlnIleI 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Probe; human; breast disease; breast cancer; development disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptide #2510 encoded by probe for measuring breast gene expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09-OCT-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAM03828 standard; Protein; 59 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              inflammatory disease; proliferative breast disease; non-carcinoma tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 LeuIleAlaAspThrHisGluValLeuValHisAspProArgValLeuGl 17
                                                                                                                                                                                                                                                                                                                             29-JAN-2001; 2001WO-US00661.
   The present invention relates to novel single exon nucleic acid probes (see AAI00010-AAI10067). The present sequence is a peptide encoded by one such probe. The probes are useful for measuring human gene expression in
                                                          Claim 27; SEQ ID No 12568; 322pp; English.
                                                                                                   Novel single exon nucleic acid probe used to measuring gene expression
                                                                                                                                 WPI; 2001-476286/51.
                                                                                                                                                                                     (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AspLeuAsnLeuGly 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ratio:
                                                                                                                                                             Hanzel DK,
                                                                                                                                                                                                                                             2000US-0608408.
2000US-0632366.
2000US-0234687.
                                                                                                                                                                                                                    2000GB-0024263.
                                                                                                                                                                                                                                                                                       2000US-0207456
                                                                                                                                                                                                                                                                                                   2000US-0180312.
                                                                                                                                                                                                                                   2000US-0236359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4.560
                                                                                                                                                                Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Identity: 76.364
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alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_block:
US-09-775-693-1/rev x AAM03828
                                                                                                                                                                                                                                                         XXX OS OS OS OS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_documentation_block:
ID AAB59826 standard; Protein; 1615 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_name: /SIDS2/gcgdata/geneseq/geneseqp/AA2001.DAT:AAB59826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Align seg 1/1 to: AAM03828 from: 1 to: 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  percent Similarity:
PN XX PD XX PF PR XX XX PR PR XX XX PI DR XX XX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   a human breast sample, where the probe hybridises at high stringency to a nucleic acid expressed in the human breast. The probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human breast, particularly those diseases with polygenic aetiology. The diseases include: breast cancer, disorders of development, inflammatory diseases of the breast, fibrocystic changes, proliferative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   breast disease and non-carcinoma tumours.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/lshed_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         573 CTCGTAGCTGATGTGCATGAGGTTCTCATCCATGCTCCACGGGTTCTTGG 524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       523 GAGTGACCGGGATGGGAATCCCGTGTTGCTTTGCGTACTCCATCAGGTCA 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     473 TTGCCGCCCTTGAACCGGTTGTAGAATTCAGGCATCCTCCAGGGAGCAAT 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      423 GACCTTTATCTGGGG 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17 uSerAspTrpAspGlyAsnProMetLeuLeuCysValPheHisGlnIleI 34
                                                                                                                                                                                                                                                                                                                                                         Toluene degradation; enzyme; waste degradation; TutE; TutD
                                                                                                                                                                                                                                                                                                                                                                                             Protein #3 encoded by TutD/E gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                04-APR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB59826;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34 leAlaAlaIleGluProValValGluLeuGlyHisProProGlySerAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 LeuIleAlaAspThrHisGluValLeuValHisAspProArgValLeuGl 17
                                                                                                                                                                                                                                                                                        Geobacter metallireducens.
                                                                                                                                                                                                                                                                                                                             Thauera aromatica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51
                                                                                                                                                                                                                                           WO200072650-A2.
                                                                                                                                                                                                                                                                            Azoarcus tolulyticus.
                                                                                                                                                                                                                                                                                                         Xanthomonas maltophilia.
                                                                                                                                      01-JUN-1999;
                                                                                                                                                                       24-MAY-2000; 2000WO-US14298
                                                                                                                                                                                                          07-DEC-2000.
                  N-PSDB; AAF23627
                                  WPI; 2001-041080/05.
                                                                  Coschigano PW;
                                                                                                     (UYOH-) UNIV OHIO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AspLeuAsnLeuGly 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      228.00
4.560
90.909
                                                                                                                                         99US-0323872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Identity: 76.364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
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ProArgArgLysThrProCyscysGlyArgThr 8 ***********************************
116TAAAGGTCATTGCTCCCTGGAGGA
SerProThrSerValSerAlaPheProProSerProAla
58 erArgI

Ν

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SX CCCCCCCCX SX PP P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X P X X
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                     alignment_scores:
                                                                                                                                                                alignment_block:
US-09-775-693-1 x AAB59813
                                                                                                                                                                                                                                                               Quality:
Ratio:
Percent Similarity:
                                                                                           Align seg 1/1 to: AAB59813 from: 1 to: 1017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1062 Cys......ArgCysLeuSerCysProGlnSerTh 1071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1050 roArgThr......CysArgAlaThrSerSerSerAlaSer 1061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1073 TGTACATCCTCGGCCGGGAGTCCCCCACTGTCTC......TCTAC 1110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1111 AATGAGGAGCTGG 1123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1071 rThrAlaAlaTrp 1075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB59813 standard; Protein; 1017 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB59813;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Toluene degradation; enzyme; waste degradation; TutD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TutD protein #4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Xanthomonas maltophilia.
Geobacter metallireducens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24-MAY-2000; 2000WO-US14298.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-DEC-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200072650-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Azoarcus tolulyticus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Thauera aromatica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to toluene degrading enzyme genes and proteins tuth (see AAF23629 and AAB59831), tutl (AAF23630 and AAB59832), proteins tuth (see AAF23629 and AAB59833), and tuth (AAF23632 and AAB59834). The tuth (AAF23631 and AAB59834) are toluene degrading enzymes are useful for biological treatment of organic toluene degrading enzymes are useful for biological treatment of organic compounds and in particular for the degradation of toluene and its analogs contained in liquid or solid waste source. The present sequence analogs contained in liquid or analogs contained in liquid or solid waste source. The present sequence is a marting sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Composition comprising toluene degrading enzyme useful for biological treatment of organic compounds, especially for degrading toluene or its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Coschigano PW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (UYOH-) UNIV OHIO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Fig 5; 122pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAF23625, AAF23627.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         is a protein sequence for toluene degrading enzyme, TutD
                         38 GCGGCCTGGACACCTCGTGCATCCTCGTGTGGCTGAAGGAACAAGGCTAT 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2001-041080/05
1017 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9905-0323872.
                                                                                                                                                                                                                                                                          193.00
0.910
42.656
                                                                                                                                                                                                                                                                             Percent Identity: 23.944
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seq_name: /SIDS2/gcgdata/geneseq/geneseqp/AA1999.DAT:AAW87504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_documentation_block:
Daggett LP,
                                    (SIBI-) SIBIA NEUROSCIENCES INC
                                                                                          20-APR-1994;
20-APR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1095 CCCACTGTCTC......TCTACAATGAGGAGCTGG 1123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1045 GTGCAGGTGTCCGTCCTCAAGGGCCCAGGTGTACATCCTCGGCCGGGAGTC 1094
                                                                                                                                                           20-APR-1994;
                                                                                                                                                                                                         15-DEC-1998.
                                                                                                                                                                                                                                                                                                                                                  Human; N-methyl-D-aspartate receptor; NMDAR2C
                                                                                                                                                                                                                                                                                                                                                                                    Human N-methyl-D-aspartate receptor subunit encoded by clone NMDA24.
                                                                                                                                                                                                                                                     US5849895-A.
                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                    NMDA-activated cation-selective ion channel; glutamate receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 465 ..ArgCysLeuSerCysProGlnSerThrThrAlaAlaTrp 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                23-FEB-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW87504;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW87504 standard; Protein; 1061 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 455 .CysArgAlaThrSerSerSerAlaSerCys.......464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           443 AsnMetArgSerThrSerValSerAlaProArgThr........... 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         995 AATTTGTCCGCCACTGCATCGCCAAGTCCCAGGAGCGAGTGGAAGGGGAAA 1044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   426 erArgArgSerProSerArgMetPheGlyArgLeuSerAlaSerSerIle 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            957 GCTGGTGTATACCG.....GTTTACGGC.....CTAGCCCTGAGTGTG 994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          410 rThrGlyArgThrProThrCysAsnSerAlaArgArg...ProValIleS 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        908 ACCGGGAAGTGCGCAAAATCAAACAAGGCCTGGGCTTGAAATTTGCTGA 956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  394 AlaGlnSerSerArgProSerCysTrpLysSerArgSerMetThrAlaTh 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      881 ATTTAGACATCGAGGCCTTCACCATGG.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       831 GTCCCGAGGTATCTACGAGACCCCCAGCAGGCACCATCCTTTACCATGCTC 880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   366 oThrThrGlySerThrCysCysAlaCysArgProAlaSer...... 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               781 CATGGCGTGGGCCGTATTGACATCGTGGAGAACCGCTTCATTGGAATGAA 830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           350 AsnThrProSerSerAlaSerThrAlaThrAlaProProThrArgLysPr 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           737 .....CCTCCTTGGAGCTCTTCATGTACCTGAACGAAGTCGCGGGCAAG 780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     333 spSerAlaIleArgArgSerSerThrThrArgSerAlaArgSerArgArg 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   316 gArgThrAlaArgArgArgCysAlaGlyPheSerSerAlaSerAlaThrA 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        665 .....TTCTCGAGATCGAGTTCAAAAA 686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .....ThrValAlaAlaArg...ArgLysLysProValArgLysValAla 393
Lu C;
                                                                                  94US-0231193.
93US-0052449.
                                                                                                                                                    94US-0231193.
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(AAV8280)) inserted between nucleotides 23050 and 2351, as set forth in AAV8280). The CDNA sequence is derived from clone NMDA24. The NMDAR subunits contribute to the formation of NMDA-activated cation-selective receptor subunit proteins, the nucleic acids are also useful as probes to Functional glutamate receptors can be assembled from several NMDA receptor subunit proteins of one type (homomeric) or from combinations of also comprises methods for using such receptor subunits to identify and agonists, antagonists and modulators of glutamate receptors. The present invention also comprises methods for determining whether unknown therefore is also comprises methods for determining whether unknown the function of such receptors.
    Sequence
                           protein(s) are functional as NMDA receptor subunits.
                                                                                                                                                                                                                                                                                                                         The present sequence represents a human N-methyl-D-aspartate (NMDA) receptor subunit (NMDAR). The nucleic acid sequence does not contain the 860 5'-most nucleotides, has an additional 11 nucleotides (AAV82891) between nucleotides 1300 and 1301, an additional 24 nucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 3; Columns 261-268; 203pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA encoding N-methyl-D-aspartate receptor subunit - useful for the assembly of functional glutamate receptor subunits
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAV82910.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1999-069812/06.
1061 AA;
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alignment_block: US-09-775-693-1 x AAW87504 alignment_scores: Align seg 1/1 to: AAW87504 from: 1 to: 1061 Percent Similarity: 624 sProSerTrpThrSerCysTrpLeuSerAlaGlyAlaSerThrAlaAlaS 641 352 GCCACAGGAAAGGGGAACG...ATCAGGTCCGGTTTGAGCTCAGCTGCT. 397 610 SerThrTrpSer.....ThrGlySerCysAlaThrArgCysProThrH1 624 302 AACAAGTGGAAATCGCCCAGCGGGAGGGGGCCAAGTATGTGTCCCACGGC 351 594 ..ThrCysCysTrpTrpProTrpGlyTrpProCysTrpSerSerProGly 609 252 GGACCGCTACCTCCTGGGCACCTCTCTTGCCAGGCCCTGCATCGCCCGCA 301 582 aSerTrpThrSerThrThrTrpGluAlaSerSer...... 593 568 CysGlySerGlnGlySerAlaArg.....MetArgArgThrArgAlaAl 582 202 TTTGTGGAGGAGTTCATCTGGCCGGCCATCCAGTCCAGCGCACTGTATGA 251 152 CACTGAAGCTTGGGGCCAAAAAGGTGTTCATTGAGGATGTCAGCAGGGAG 201 551 rpArgSerCysSerSerTrpGlyThrGluArgHisArgAsnTrpArgGln 105 GGCCAACATTGGCCAGAAGGAAGACTTCGAGG...AAGCCAGGAAGAAGG 151 536 rAlaSerProCys.....ArgArgThrProThrGlySerGlyProThrT 551 520 AlaSerTrpSerProLeuGlyLeuAlaArgSerLeuLeuProLeuAlaTh 536 55 TGCATCCTCGTGTGGCTGAAGGAACAAGGCTATGACGTCATTGCCTATCT 104 38 GCGGCCTGGACACCT......CG 54 Quality: Ratio: 174.00 0.961 38.593 Percent Identity: 23.881 Length:

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641 eralaGlyCysArgAlaSerProAlaHisArgGlyArgProAlaArgThr 657
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              658 SerargproalaargproargproalaCysSerArgPheCysArgGlnPr 674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     492 AAAGCAACACGGGATTC......ccaTCCCGGTCACTCCCA 526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    674 oAlaThrTrpProArgArgAlaAlaThrProTrpThrAlaProLeuAlaP 691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                451 TACAACCGGTTCAAGGGCCGCAATGACCTGATGGAGT.....ACGC 491
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            527 AGAACCCGTGGAGGATGGATGAGAACCTCATGCACATCAGCTACGAGGCT 576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              708 ArgProArgGlyLeuAlaProAlaHisAlaCysProProProThrArgPr 724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 577 GGAATCCTGGAGAACCCCAAGA.....ACCA 602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        603 AGCGCCTCCAGGTCTCTACACGAAGACCCAGGACCCAGGCCAAAG...... 646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   724 oGlnSer...ArgAlaProArgAlaGlyAspArgGlnThrGlyValAlaA 740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        740 rgargLeuCysalaGlyLeuargSerProArgAlaAlaProArgArgArg 756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               757 GlyargproCysProThrSerProGluCysArgAlaAlaGlnProGlyAr 773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         773 gArgGly......GlyArgCysGlyProGlyThrA 783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       783 laGlyGlyThrSerArgPropro...SerGlyProCysArgProArgAla 798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    758 .....ACCTG 762
                                                                                                                                                                                                                                                                                                                                                                                                                                                            799 ValThrThrAlaProPheLeuGluProThrAspProAlaAlaProSerSe 815
                                                                                                                                                                                                                                                                                                                                                                                                 815 rArgSerSerArgSerProArgSerTrpArgThrCysArgCysSerValA 832
                                                                                                                                                                                                                                                                                                                                                                                                                            832 rgSerSerTrpPro.......GlyGlyArgProCysThr 842
                                                                                                                                                                                                                                                                                                                                                                   798 TGACATCGTGGAGAACCGCTTCATTGGAATGAAGTCCCGAGGTATCTACG 847
                                                                                                                                                                                                                                                                          843 ArgPro......GlyProGlyAlaArgAlaArgValThrLeuProCysPr 857
                                                                                                                                                                                                                                                                                                        848 AGACCCCAGCAGCACCATCCTTTACCATGCTCATTTAGACATCGAGGCC 897
                                                                                                                                                                                                                857 OAlaProTrpProArg.....862
                                                                                                                                                                                                                                             898 TTCACCATGGACCGGGAAGTGCGCAAAATCAAACAAGGCCTGGGCTTGAA 947
1077 CATCCTCGGCCGGAGTCCCCACTGTCTCTCTACAATGAGGAGCTGGTGA 1126
                                                            1027 GAGCGAGTGGAAGGGAAAGTGCAGGTGTCCGTCCTCAAGGGCCAGGTGTA 1076
                                                                                                                                                  863 ......proSerLeuGlyProAla...ArgCysPro 871
                                                                                                                                                                                  948 ATTTGCTGAGCTGGTGTATACCGGTTTACGGCCTAGCCCTGAGTGTGAAT 997
                                                                                         872 LeuGlyAlabroAlabroProAlaProAlaProThrAlaThrArgProAl 888
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seq_name: /SIDS2/gcgdata/geneseq/geneseqp/AA1999.DAT:AAW87503
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                              alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human N-methyl-D-aspartate receptor subunit encoded by clone NMDA22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-FEB-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW87503;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NMDA-activated cation-selective ion channel; glutamate receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; N-methyl-D-aspartate receptor; NMDAR2C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-DEC-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US5849895-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                  The present sequence represents a human N-methyl-D-aspartate (NMDA) The nucleic acid sequence does not contain receptor subunit (NMDAR). The nucleic acid sequence does not contain the 366 5'-most nucleotides by the insertion of 11 nucleotides between nucleotides 1300 and 1301, nor the 15 nucleotides at positions the 1960-1974, nor the 1061 3' nucleotides, as set forth in AAV82889. The nucleotides is derived from clone NMDA21. The NMDAR subunits contribute to the formation of NMDA-activated cation-selective ion channels. In addition to being useful for the production of NMDA receptor subunit to to being useful for the production of NMDA receptor subunit proteins, the nucleic acids are also useful as probes to identify and isolate nucleic acids encoding related receptor subunits. Functional proteins, the nucleic acids encoding related receptor subunits. Functional places are also useful as probes to identify and proteins of one time of the production of NMDA receptor subunit isolate nucleic acids encoding related receptor subunits. Functional proteins of one time of the production of NMDA receptor subunit isolate nucleic acids encoding related receptor subunits.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20-APR-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         assembly of functional glutamate receptor subunits
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA encoding N-methyl-D-aspartate receptor subunit - useful for the
                                                                                                                                               proteins of one type (homomeric) or from combinations of submit proteins of different types (heteromeric). The present invention also comprises of different types (heteromeric). The present invention also comprises methods for using such receptor subunits to identify and characterise methods for using such receptor subunits to receptors, e.g. agonists, compounds which affect the function of such receptors, e.g. agonists, antagonists and modulators of glutamate receptor function. The invention also comprises methods for determining whether unknown protein(s) are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 3; Columns 253-262; 203pp; English.
                                                                                          sequence 1212 AA;
                                                                                                                                  functional as NMDA receptor subunits
Quality: 174.00
Ratio: 0.961
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93US-0052449.
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Seq. XX	ν Φ
AAB26240 standard; Protein; 1081 AA. AAB26240; 23-FEB-2001 (first entry) Human N-methyl-D-aspartate receptor subunit NMDARIA; ionotropic; glutamate receptor; drug screening; animal model; disease diagnosis; misc-difference 116 //label= unknown Misc-difference 140 //label= unknown //label= unknown //label= unknown //label= unknown //label= unknown	924 9ArgGly

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Misc-difference
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        Novel DNA fragment encoding human N-methyl-D-aspartate receptor subunit for identifying mutations and for developing drugs against various disease states
                                                          Daggett LP,
                                                                                         20-APR-1994;
20-APR-1993;
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       disease states
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/note= "encoded;
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593..594
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number of in-frame stop codons which are represented
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US-09-775-693-1 x AAB26240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence is a subunit (designated NMDARIA) of the human N-methyl-D-aspartate (NMDA) receptor. This is an ionotropic glutamate receptor which contains cation-specific ligand-gated ion channels. The protein and its coding sequence can be used in disease diagnosis and in research to identify other, similar proteins. They can also be used as probes, for example in genetic screening, and in drug screening, as well as enabling the production of animal disease models.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            681
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                                                                                                                                                                                                                                                                                                                                                                                                                   367 AACGATCAGGTCCGGTTTGAGCTCAGCTGCTACTCACTGGCCCCCCAGAT
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  593 CCAAGA
                                          729 laProAlaHisAlaCysProProThrArgProGlnSer...ArgAla
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                                                                               GGATGAGAACCTCATGCACATCAGCTACGAGGCTGGAATCCTGGAGAACC
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                                                                                                                                                              C.....CCATCCCGGTCACTCCCAAGAACCCGTGGAGCAT
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	TGATTATGAGCCAACTGATGCCACCGGGTTCATCAACATCA 1183	143
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87		879
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87	oGlyAlaArgAlaArgValThrLeuProCysProAlaProTrpProArg	863
91	GCCTTCACCATGGACCGGG	864
86	*ThrArgProGlyP	853
86	PACGAGACCCCAGCAGGCAC	814
80	G1	837
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75	CCTCCTTGGAGCTCTTCATGT	736
80	GlyArgCysGlyProGlyThrAlaGlyGlyThrSerAr	792
73		701
79	aAlaGlnProGlyArgArgG	778
7(651
77	ArgArgGlyArgProCys	761
6	TACACGAAGACCCAGGACCCAGCCAAAG	619
76	${\tt ProArgAlaGlyAspArgGlnThrGlyValAlaArgArgLeuCysAlaGl}$	745

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Database sequences: 21225
Database length: 22503292
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Command line parameters:
               /cgn2_6/ptcodata/2/iaa/5A_COMB.pep:US-08-963-825-19 + 110.50 157.93 0.0 (cgn2_6/ptcodata/2/iaa/5A_COMB.pep:US-08-642-255-62 + 116.00 167.05 0.0070 (cgn2_6/ptcodata/2/iaa/6A_COMB.pep:US-08-963-825-18 + 116.00 164.22 0.0080 (cgn2_6/ptcodata/2/iaa/6A_COMB.pep:US-08-931-820-1 + 113.00 161.78 0.0139 (cgn2_6/ptcodata/2/iaa/6A_COMB.pep:US-08-931-820-1 + 113.00 161.78 0.0139 (cgn2_6/ptcodata/2/iaa/6A_COMB.pep:US-08-931-820-4 + 113.00 161.78 0.0139 (cgn2_6/ptcodata/2/iaa/6A_COMB.pep:US-09-035-648-24 + 111.50 163.48 0.0159 (cgn2_6/ptcodata/2/iaa/6A_COMB.pep:US-09-035-648-24 + 111.50 153.48 0.0159 (cgn2_6/ptcodata/2/iaa/6A_COMB.pep:US-08-931-820-2 + 110.50 157.71 0.0241 (cgn2_6/ptcodata/2/iaa/6A_COMB.pep:US-08-963-825-19 + 110.50 154.18 0.0284 (cgn2_6/ptcodata/2/iaa/6A_COMB.pep:US-08-863-825-19 + 110.50 152.99 0.0203 (cgn2_6/ptcodata/2/iaa/6A_COMB.pep:US-08-863-825-19 + 110.50 162.99 0.0203 (cgn2_6/ptcodata/2/iaa/6A_COMB.pep:US-08-8687A-49 + 110.00 162.99 0.0203 (cgn2_6/ptcodata/2/iaa/6A_COMB.pep:US-08-96887A-49 + 110.00 162.93 0.0203 (cgn2_6/ptcodata/2/iaa/6A_COMB.pep:US-08-919-887A-49 + 110.50 154.04 0.0412 (cgn2_6/ptcodata/2/iaa/6A_COMB.pep:US-08-919-887A-49 + 108.50 161.83 0.0266 (cgn2_6/ptcodata/2/iaa/6A_COMB.pep:US-08-919-887A-49 + 108.50 161.91 0.0266 (cgn2_6/ptcodata/2/iaa/6A_COMB.pep:US-08-919-887A-49 + 108.50 161.91 0.0266 (cgn2_6/ptcodata/2/iaa/6A_COMB.pep:US-08-919-897-919-897-919-897-919-897-919-897-919-897-919-897-919-897-919-897-919-897-919-897-919-897-919-897-919-897-919-897-919-897-919-897-919-897-919-897-919-897-919-897-919-897-919-897-919-897-919-897-919-897-919-897-919-897-919-897-919-897-919-897-919-897-919-897-919-897-919-897-919-897-919-897-919-897-919-897-919-897-919-897-919-897-919-897-919-897-919-897-919-897-919-897-919-897-919-897-919-897-919-897-919-897-919-897-919-897-919-897-919-897-919-897-919-897-919-897-919-897-919-897-919-897-919-897-919-897-919-897-919-897-919-897-919-897-919-897-919-897-919-897-919-897-919-897-919-897-919-897-919-897-919-897-919-897-919-897-919-897-919-897-919-897-919-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /cgn2_6/ptodata/2/laa/6B_COMB.pep:US-09-219-849-49 + 118.00
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/cgn2_6/ptodata/2/laa/5A_COMB.pep:US-08-642-255-80 + 116.50
/cgn2_6/ptodata/2/laa/6A_COMB.pep:US-08-642-246-16 + 116.50
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-Q=/cgn2_1/USPTO_spool/US09775693/runat_12022002_124152_1324/app_query.fasta_1.1315
-DB=-Tssued_patents_AA -QFMT=fastan -SUFFIX=ra1 -GAPOP=12.000
-GAPEXT=4.000 -MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000
-QGAPOP=4.500 -QGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500
-FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
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-USER=US09775693_@CGN1_1_22 -NCPU=6 -ICPU=3 -LONGLOG -NO_XLPXY
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-THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs
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_6/ptodata/2/iaa/6A_COMB
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sequences: 212252
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3.1e-05
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:US-08-525-742-6 + 105.50
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SEQ ID NO 7
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seq_name: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-09-219-849-7
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US-09-775-693-1 x US-09-219-849-7
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    Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/219,849
CURRENT FILING DATE: 1998-12-23
NUMBER OF SEQ ID NOS: 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: WIND, RICHELE D.
APPLICANT: VAN DEN BOSCH, TANJA J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Description of Artificial Sequence: Illustrative OTHER INFORMATION: amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                      114 SerArgAspProGlyProProGlyAlaHisGlyProAlaGlyProLysGl
                                                                                                                                                                                                                                                                                                                                                                         130 y......AlaHisGlyProAlaGlyProLysGlyAlaHisG
419 AGGTCATTGCTCCCTGGAGGATGCCTGAATTCTACAACCGGTTCAAGGGC
                                       178 ro.AlaGlyProGlyGlySerArg.....AspProGlyProProGly..
                                                                                                                    161 oAlaGlyProGlyGlySerArgAspProGlyProProGlyAlaGlnGlyP 178
                                                                                                                                                               319 CAGCGGGAGGGGCCAAGTATGTGTCCCACGGCGCCACAGGAAAGGGGAA
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                                                                            CGATCAGGTCCGGTTTGAGCTCAGCTGCTACTCACTGGCCCCCAGATAA 418
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VAN RIJW, ALEXIS C.
BOUWSTRA, JAN B.
DE WOLF, FREDERIK A.
MOOBROEK, ANDREAS
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5 0.0509
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0.0386
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seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 6, Application US/09219849 Patent No. 6150081
   APPLICANT: VAN HEERDE, GEORGE V.
APPLICANT: VAN RIJN, ALEXIS C.
APPLICANT: BOUWSTRA, JAN B.
APPLICANT: BOUWSTRA, JAN B.
APPLICANT: MOOBROEK, ANDREAS
APPLICANT: WERTEN, MARC W.T.
APPLICANT: WIND, RICHELE D.
APPLICANT: WIND, RICHELE D.
APPLICANT: VAN DEN BOSCH, TANJA J.
TITLE OF INVENTION: SILVER HALIDE EMULSIONS WITH RECOMBINANT COLLAGEN
TITLE OF INVENTION: PREPARATION THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1048 CAGGTGTCCGTCCTCAAGGGCCAGGTGTACATCCTCGGCCGGGAGTCCCC 1097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          333 ......ProAlaGlyProGlyGlySerArgAspProGlyProPro 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        998 TTGTCCGCCACTGCATCGCCAAGTCCCAGGAGCGAGTGGAAGGGAAAGTG 1047
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            283 GlyProLysGly.....AlaHisGlyProAlaGlyProLysGlyAlaGl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               698 TGAAGGTGACCAACGTCAAGGATGGCACCACCCACCAGACCTCCTTGGAG 747
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 208 GlyAlaGlnGlyProAlaGlyProGly.....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .GlySerArgAspProGlyProProGlyAlaGlnGlyProAlaGlyProG 233
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2728-2
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; OTHER INFORMATION: Description of Artificial Sequence: Illustrative ; OTHER INFORMATION: amino acid sequence US-09-219-849-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Align seg 1/1 to: US-09-219-849-6 from: 1 to:
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SEQ ID NO 6
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CURRENT FILING DATE: 1998-12-23
NUMBER OF SEQ ID NOS: 50
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TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                347 lyProAlaGlyProGlyGlySerArg......AspProGlyPro
683 AAAAAGGGGTCCC.....TGTGAAGGTGACCAACGTCAAGGATGGCACC 726
                                                     360 ProGlyAlaGlnGlyProAlaGlyProGlyGlySerArgAsp..... 373
                                                                                                                                                                                                                                                                                  330 yProAlaGlyProGlyGlySerArgAspProGlyProProGlyAlaGlnG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           297 roAlaGlyProGlyGlySerArgAspProGlyProProGlyAlaGlnGly 313
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                                                                                                              .....AGCCAAAGCCCCCAACACCCCTGACATTCTCGAGATCGAGTTCA 682
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Gaps: 20
Percent Identity: 26.050
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   Patent No. 5852187
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                                                                                                                  GENERAL INFORMATION:
APPLICANT: Thorner, Michael O.
APPLICANT: Gaylinn, Bruce D.
APPLICANT: Horikawa, Reiko
APPLICANT: Lyons Jr., Charles E.
TITLE OF INVENTION: MOLECULAR CLONING OF THE OVINE PITUITARY
TITLE OF INVENTION: GROWTH HORMONE RELEASING HORMONE RECPTOR
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1135 GTGCAGGG 1142
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STREET: G. Street CITY: Washington STATE: D.C.
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571 SerSerThrSerGlnGlySerTyr.......ProCysSerHisProSe 584
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TAAAGGTCATTGCTCCCTGGAGGATGCCTGAAT 448	410CCCAGATAAAGGTCATTG
${ t lyThrAlaProLeuGlnAlaGlyArgSerProSet}$	yThrAlaPro
:	
<pre>PCAGGTCCGGTTTGAGCTCAGCTGCTACTCACTGGCC 408 </pre>	AGGT
GGGCC GlyTh	04 laproGlySerGlyTh
	9 sValTyrLysLeuLeuLysGly
Mecserserleuse MGGCCCTGCATCGC	2CCTCTCTTGCCAGGCCCT
2	
TCCAGCGCACTGTATGAGGACCGCTACCTCC SerAlaCysTrpAlaProCysGlnSerSer	22 GCCGGCCATCCAGTCCAGCGCACT
TCAGCAGGAGTTTGTGGAGGAGTTCATCTG 221 :::::::: ::::: AlaValAlaGluLeuProProTrpAlaAlaGlyCysG 56	/8 TTCATTCAAGATGTCAGCAGGGAGT
CCAGGAAGAAGGCACTGAAGCTTGGGGCCAAAAAGGTG 17: 1yG1yArgSerThrGlyProProArgLe 40	28 ACTTCGAGGAAGCCAGGAAGAAGGC ::: 27 ThrThrGlyAspGlyGlyArg
s-08-660-963-12 from: 1 to: 498	to: US-08-660-963-
-08-660-963-12	8-660-963-1
137.50 Length: 437 0.795 Gaps: 25 39.588 Percent Identity: 22.197	37.50 .795 9.588 Per
ear protein	TOPOLOGY: linear MOLECULE TYPE: protei 5-08-660-963-12
o aci	LENGTH: 498 amino acid TYPE: amino acid
O ID NO: 12: ERISTICS:	INFORMATION FOR SEQ ID NO: 12 SEQUENCE CHARACTERISTICS:
824-8199	TELEFAX: 202-8: TELEFAX: 202-8:
TION 1	REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMAT
With the stand P. With the standard sta	NAME: O'Shaughnessy, Bria REGISTRATION NUMBER: 32,7
Z '	CLASSIFICATION: 536 ATTORNEY/AGENT INFORMATION
MBER: US/08/660,963 12-JUN-1996	CATION NUMBER: US/08 G DATE: 12-JUN-1996
PC-DOS/M	OPERATING SYSTEM: PC-DOS SOFTWARE: Patentin Relea
Floppy disk PC compatible	MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatib
	COUNTRY: USA ZIP: 20005 COMPUTER READABLE FORM.

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153 rgLeuIleProArg...ProAlaLeuCysProTrpSerCysLeuArgArg 168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 169 AsnProThrSerProArgGlySerSerThrProTrpAlaThrAlaSerAr 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              449 TCTACAACCGGTTCAAGGGCCGCAATGACCTGATGGAGTACGCAAAGC... 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             543 GGATGAGAACCTCATGCACATCAGCTACGAGGCTGGAATCCTGGAGAACC 592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               185 gLeuGlnProSerTrpProSerSerSerTrpSerLeuSerGlyGly.... 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                678 GTTCAAAAAAGGGGTCCCTGTGAAGGTGACCAACGTCAAGGATGGCACCA 727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               231 rGlyArgThrTrpThrThrAlaAlaSerProLeuSer ..... 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            632 ....AGGACCCAGCCAAAGCCCCCAACACCCCTGACATTCTCGAGATCGA 677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ||| ::::::||| |||::: :::||| ||| 231
215 ProLeuSerSerArgArgGlnLeuCysSerArgThrProProSerPheTh 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              593 CCAAGAACCAAGCGCCTCCAGGTCTCTACACGAAGACCC......631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              201 ......SerThrAlaProGlyThrThrSerThrProSerCysSerPro 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           244 .....CysAlaArgLeuLeuPro 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 250 ProLeuIleSerArgProProThrSerAlaGlyCysTrpGlnLysLeuCy 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                283 lyTrpPheSerLeuProGlyGlyPheLeuCysSerSerProAlaCysGly 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             770 .....TCGCGGGCAAGCATGGCG 787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  266 sThrProAlaSerProProHisCysProAlaGlnGlyGlySerSerGlyG 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               757 TACCTGAACGAAG...... 769
                                                                                                                                            1039 GGGAAAGTGCAGGTGTCCGTCCTCAAGGGCC.....AGGTGTA 1076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               838 GGTATCTACGAGACCC......CAGCAGGCACCATCC..... 868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              300 Trp.....ValAlaSerTrpProLeuLysMetLeuArgAlaGlyThrTr 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              788 TGGGCCGTATTGACATCGTGGAGAACCGCTTCATTGGAATGAAGTCCCGA 837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             331 euLeuGlyThrLeuGlyPhePheSerIleLeuSerValSerCysGlyAsn 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             314 pThrThrAlaProProThrGlyGlySerSerLysAspProSerSerSerL 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           869 TTTACCATGCTCATTTAGACATCGAGGCCTTCACCATGGACCGGG..... 913
                                               1077 CATCCTCGGCC 1087
                                                                                                                                                                                                                                                                                                                                                                                               364 rLeuSerGlnArgPheSerSerPheArgCysLeuGluSerThrMetSerP 381
                                                                                         401 .....AlaLeuSerArgAlaSerLeuLeuLeuSerCysT 412
                                                                                                                                                                                           391 ......TrpThrSerAlaSerProAsnTrpAspTrp.. 400
                                                                                                                                                                                                                                             989 AGTGTGAATTTGTCCGCCACTGCATCGCCAAGTCCCAGGAGCGAGTGGAA 1038
                                                                                                                                                                                                                                                                                          381 heSer......ThrSerCysLeuThrValLeuGly...... 390
                                                                                                                                                                                                                                                                                                                                             939 GGGCTTGAAATTTGCTGAGCTGGTGTATACCGGTTTACGGCCTAGCCCTG 988
412 hrAlaserser 415
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seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT ; ORGANISM: Sorangium cellulosum US-09-413-814-78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 78, Application US/09413814 patent No. 6225064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_block:
US-09-775-693-1 x US-09-413-814-78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Align seg 1/1 to: US-09-413-814-78 from: 1 to: 882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/413,814
CURRENT FILING DATE: 1999-10-07
EARLIER APPLICATION NUMBER: DE 198 46 493.2
EARLIER FILING DATE: 1998-10-09
NUMBER OF SEQ ID NOS: 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Dougherty, Brian A
APPLICANT: Goldberg, Steven L
APPLICANT: Hofie, Gerhard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: DNA sequences for enzymatic synthesis of polyketide or TITLE OF INVENTION: heteropolyketide compounds FILE REFERENCE: PCT/US 99/23535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Mueller, Joachim APPLICANT: Reichenbach, Hans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Bloecker,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   107 CCAACATTGGCCAGAAGGAAGACTTCGAGGAAGCCAGGAAGAAGCCACTG 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          157 AAGCTTGGGGCCA...AAAAGGTGTTCATTGAGGATGTCAGCAGGGAGTT 203
                                                                                                                                                                                                                                                                                                                                                                                                                                    204 TGTGGAGGAGTTCATCTGGCCGGCCATCCAGT.....CCAGCGCACTGT 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             373 .....SerProArgArgArgProSerProSerAlaArgSerProAlaI 387
                                                                                                                                                                                                                                                                                                    404 LeuArgProAlaArgArgLeuAlaArgArgAspProGlyAspValProAs 420
                                                                                                                                                                                                                                                                                                                                              248 ATGAGGACCGCTACCTCCTGGGCACCTCTCTTGCCAGGC......CCTGC 291
                                                                                                                                                                                                                                                                                                                                                                                            387 leTrpGluArgProProArgArgProArgAspArgProArgProArgLeu 403
                                         450 AlaProArgArgGly......AlaAlaAlaArg.ValProProAspA 463
                                                                                                                             437 laAspGlyArgGly......AlaArgGlyProGlyArgArgArg 449
                                                                                                                                                                       323 .....GGGAGGGGCCAAGTATGTGTCCCACGGCGCCACAGGAAAGGGGA 367
                                                                                                                                                                                                                420 pProArgAlaAlaArgArgAlaProAlaAlaGlyAlaLeuProGlyA 437
                                                                                                                                                                                                                                                             368 ACGATCAGGTCCGGTTTGAGCTCAGCTGCTACTCACTGGCCCCCCAGATA 417
418 AAGGTCATTGCTCCCTGGAGGATGCCTGAATTCTACAACCGGTTCAAGGG 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         882
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Beyer, Stefan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bristol-Myers Squibb, Co.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cino, Paul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           134.00 Length: 433
0.784 Gaps: 24
39.492 Percent Identity: 25.173
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YATGATGALAVALPROGLYATGATGATGATGATGATGATGATGATGATGATGATGATGA	468 CCGCAATGACCTGATGATGATGATGATGACGAAAGCAAC 476 ArgAlaAlaProAlaValValArgArgSerAl 518 TCACTCCCAAGAACCCGTGGAGGAGCATGAATGATGAC 492 yValGln
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306 AGTGGAAATCGCCCAGCGGGAGGGGGCCAAGTATGTGTCCCACGGCGCCA 355	256 CGCTACCTCCTGGGCACCTCTCTTGCCAGGCCCTGCATCGCCCCGCAAACA 305	206 TGGAGGAGTTCATCTGGCCGGCCATCCAGTCCAGCGCACTGTATGAGGAC 25	Align seg 1/1 to: US-08-483-533-41 from: 1 to: 355	alignment_block: US-09-775-693-1 x US-08-483-533-41	alignment_scores: Quality: 131.50 Length: 343 Ratio: 1.035 Gaps: 19 Percent Similarity: 37.026 Percent Identity: 24.490	83-533 igenic Tive 25	704ProProAspGlnGly 708
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	5 CCGGGAGTCCCCACTGTCTCTACAA 1112 ::: ::: 3 ProGlyMetValIleLysAsnLeuGln 346	338 338
		Ñ,
	CCTCAAGGGCCAGGTGTACATCCTCG	Ū
32	::: ::: ::: dGlnArqGlyGlyAlaArqProThrSerValArqArqValPheGlyAla	0
10	GGAAAGTGCAGGTGTCCGT	1040
30		290
10	GTGTGAATTTGTCCGCCACTGCATCGCCAAGTCCCCAGGAGCGAGC	990
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98	GGCTTGAAATTTGCTGAGCTGGTGTATACCGGCTTTACGGCCTAGCC	940
27	::: ::: ::: AlaProGlySerSerAlaProSerAr	259
93	TCGAGGCCTTCACCATGGACCGGGAAGTGCGCAAAATCAAACAAGGCC	890
25	::: gSerAsnValThrPro	245
88	GAGACCCCAGCAGGCACCATCCTTTACCATGCTCATT	840
24,	ArgProValProGlyProTrpProAlaGluP	231
839	GCCGTATTGACATCGTGGAGAACCGCTTCATTGGAATGAAGTCCCGAGG	790
23	pArgArgProArgArgSerSerGlyArgAlaTr	215
789	TGAACGAAGTCGCGGGCAAGCATGGCGTG	759
215	:::::: ::: pArgAlaAla.AlaArgGlyProAlaSerGlyPi	199
758	AGCTCTTCATGTA	744
199	 hrSerGlyCysAlaThrTrpTrpSerGlyProArgProProAla	183
743	CAACGTCAAGGATGGCACCA	706
182		
705	CCCTGACATTCTCGAGATCGAGTTCAAAAAAGGGGTCCCTGTGAAGGTG	656
171	SerProProArgProProArgProProArgProProArg	158
655	CCTCCAGGTCTCTACACGAAGACCCAGGACCCAGCCAAAGCCCCCCAACA	909
158	AspAlaArgAlaGlyArgGlyArgA	148
509	TGCACATCAGCTACGAGGCTGGAATCCTGGAGAACCCCAAGAACCAAGC	556
148	::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::: ::::: ::: :::: :::: ::: :::: ::: :::: :::: :::: ::: ::: :::	140
555	GTGGAGCATGGATGAGAACCTC	506
139		139
505	CCGGTTCAAGGGCCGCAATGACCTGATGGAGTACGCAAAGCAACACGGGA	456
139	 SerAlaPheArgArgAlaSerProSerAlaCysAlaSer	126
455	CCCCCAGATAAAGGTCATTGCTCCTGGAGGATGCCTGAATTCTACAA	406
125	ArgAla	124
405		356
T 2 2	TrpAlaArgGlyAlaGlyLeuThrProProThrProPro	TTT

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seq_documentation_block:
    Sequence 3, Application PC/TuS9106532
    GENERAL INFERMATION:
    APPLICANT: Roizman, Bernard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US91-06532-3
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Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_block:
us-09-775-693-1 x PCT-US91-06532-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Gruber, Lewis S.
REGISTRATION NUMBER: 30,060
REFERENCE/DOCKET NUMBER: 2737:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/346-5750
TELEFAX: 312/984-9740
TELEFAX: 312/984-9740
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 355 anino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Align seg 1/1 to: PCT-US91-06532-3 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Rec
TITLE OF INVENTION: Vac
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                     111 ..TrpAlaArgGlyAlaGlyLeuThrPro.....ProThrProPro 123
                                                                                                                                                                                                                                                                                                                                                                                                                             206 TGGAGGAGTTCATCTGGCCGGCCATCCAGTCCAGCGCACTGTATGAGGAC 255
  126
                                            406 GCCCCCCAGATAAAGGTCATTGCTCCCTGGAGGATGCCTGAATTCTACAA 455
                                                                                       124 ArgAla..... 125
                                                                                                                                                                                                                                    306 AGTGGAAATCGCCCAGCGGGAGGGGGCCCAAGTATGTGTCCCACGGCGCCA 355
                                                                                                                                                                                                                                                                                                                                   256 CGCTACCTCCTGGGCACCTCTCTTGCCAGGCCCTGCATCGCCCGCAAACA 305
                                                                                                                                           356 CAGGAAAGGGGAACGATCAGGTCCGGTTTGAGCTCAGCTGCTACTCACTG 405
                                                                                                                                                                                                                                                                                    82 TrpProAspSerProProProGluSerAlaProGlu......AlaAr 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: PCT/US91/06532 FILING DATE: 19910910 CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & ADDRESSEE: Bicknell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET:
.ProSerAlaPheArgArgAlaSerProSerAlaCysAlaSer..... 139
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1.035
37.026
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Identity: 24.490
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	<pre>seq_documentation_block: Sequence 72, Application US/08642255 Patent No. 5773249 GENERAL INFORMATION: APPLICANT: CAPPELLO, Joseph APPLICANT: FERRARI, Franco A.</pre>
	<pre>seq_name: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:US-08-642-255-72</pre>
	1086 CCGGGAGTCCCCACTGTCTCTCTACAA 1112 ::: 338 ProGlyMetVallleLysAsnLeuGln 346
1085 337	AAGGGCCAGGTGTACATCCTCGG :: snGlyProGlyArgProLeu
1058 322	40 GGAAAGTGCAGGTGTCCGT
1039 305	0 GTGTGAATTTGTCCGCCACTGCATCGCCAAGTCCCAGGAGCGAGTGGAAG
989 289	940 GGCTTGAAATTTGCTGAGCTGGTGTATACCGGTTTACGGCCTAGCCCTCA ::: :: ::
939 273	890 TCGAGGCCTTCACCATGGACCGGGAAGTGCGCAAAATCAAACAAGGCCTG
889 259	840 TATCTACGAGACCCCAGCAGCACCATCCTTTACCATGCTCATTTAGACA
839 244	790 GGCCGTATTGACATCGTGGAGAACCGCTTCATTGGAATGAAGTCCCGAGG 231 lyproArgproValproGlyproTrpproAlaGluproAla
789 231	759CTGAACGAAGTCGCGGGCAAGCATGGCGTG :::
758 215	744 GGAGCTCTTCATGTA
743 199	706 ACCAACGTCAAGGATGGCACCACCCACCAGACCTCCTT
705 182	656 CCCCTGACATTCTCGAGATTCAAAAAAAAGGGGTCCCTGTGAAGGTG
655 171	606 GCCTCCAGGTCTCTACACGAAGACCCAGGACCCAAGCCAAAGCCCCCAACA
605 158	556 ATGCACATCAGCTACGAGGCTGGAATCCTGGAGAACCCCAAGAACCAAGC : ::: ::: ::: :::
555 148	506 TTCCCATCCCGGTCACTCCCAAGAACCCGTGGAGCATGGATGAGAACCTC
139	139
505	456 CCGGTTCAAGGGCCGCAATGACCTGATGGAGTACGCAAAGCAACACGGGA

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alignment_block: US-09-775-693-1 x US-08-642-255-72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-642-255-72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (415) 494-8771
TELEX: 910 277299 FHT UR
INFORMATION FOR SEQ ID NO: 72:
SEQUENCE CHARACTERISTICS:
371 ATCAGGTCCGGTTTGAGCTCAGCTGCTACTCGCCCCCCGGATAAAG 420
                                                                     355 lyProProGlyAlaGlnGlyProAlaGlyProGlyGlySerArgGlyAsp 371
                                                                                                             330 GGCCA.....AGTATGTGTCCCACGGCGCCA...CAGGAAAGGGGAACG 370
                                                                                                                                                              338 oProGlyAlaGlnGlyProAlaGlyProGlyGlySerArgGlyAspProG 355
                                                                                                                                                                                                             280 GCCAGGCCCTGCATCGCCCGCAAACAAGTGGAAATCGCCCAGCGGGAGGG 329
                                                                                                                                                                                                                                                             322 GlyAlaGlnGlyProAlaGlyProGlyGlySerArgGlyAspProGlyPr 338
                                                                                                                                                                                                                                                                                                       243 ACTGTATGAGGACCGCTACCTCCTGGGCA.......CCTCTCTT 279
                                                                                                                                                                                                                                                                                                                                                        305 laGlnGlyProAlaGlyProGlyGlySerArgGlyAspProGlyProPro 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                          193 AGCAGGGAGTTTGTGGAGGAGTTCATCTGGCCGGCCATCCAGTCCAGCGC 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                       292 ......GlyProLysGlyAlaHisGlyProAlaGlyProLysGlyA 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      277 GlyAlaHisGlyProAlaGlyPro...LysGlyAlaHisGlyProAla.. 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    105 GGCCAACATTGGCCAGAAGGAAGACTTCGAGGAAGCCAGGAAGAAGAAGCCAC 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: A55556-3/BIR TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 494-8700
TELEPHONE: (415) 494-8771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: ROWLAND, Bertram I.
REGISTRATION NUMBER: 20,015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/642, 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET:
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: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1065 amino acids
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0.818
40.050
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Gaps: 27
Percent Identity: 28.463
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seq_name: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:US-07-945-283-2
seq_documentation_block:

; MOLECULE TYPE: protein US-07-945-283-2 alignment_block: US-09-775-693-1 x US-07-945-283-2 alignment_scores: Align seg 1/1 to: US-07-945-283-2 from: 1 to: 1958 Sequence 2, Application US/07945283 Patent No. 5352596 GENERAL INFORMATION: percent Similarity: TELEFAX: 309-685-4128 INFORMATION FOR SEQ ID NO: 2: CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtis P. Ribando
STREET: 1815 No. 5352596th University Street APPLICANT: Cheung, Andrew K.
APPLICANT: Wesley, Ronald D.
TITLE OF INVENTION: Pseudoorabies Virus Deletion Mutants
TITLE OF INVENTION: Involving The EPO and LLT Genes TELECOMMUNICATION INFORMATION: TELEPHONE: 309-685-4011 ext.513 ATTORNEY/AGENT INFORMATION: NAME: Ribando, Curtis P COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy SEQUENCE CHARACTERISTICS: LENGTH: 1958 amino aci CURRENT APPLICATION DATA NUMBER OF SEQUENCES: 349 HisGlnAspProProGlyGlyProProSerAlaGluThrHisHisHi 365 468 CCGCAATGACCTGATGGAGTACGCAAAGCAACACGGGATTCCCATCCCGG 517 421 GTCATTGCTCCCTGGAGGATGCCTGAATTCTACAACCG...GTTCAAGGG 467 371 ATCAGGTCCGGTTTGAGCTCAGCTGCTACTCACTGGCCCCCCAGATAAAG 420 321 ro.....GlyProProThrProSerThrSer.HisHisHisHisHisHi 335 321 GCGGGAGGGGCCAAGTATGTGTCCCACGGCGCCACAGGAAAGGGGAACG 370 271 ACCTCTTTGCCAGGCCCTGCATCGCCCGCAAACAAGTGGAAATCGCCCA 320 297 GlyProProSerSerAsnSerHis..... 221 GGCCGGCCATCCAGTCCAGCGCACTGTATGAGGACCGCTACCTCCTGGGC 270 STREET: CITY: P NAME: Ribando, Curtis P REGISTRATION NUMBER: 27976 FILING DATE: 1: CLASSIFICATION: OPERATING SYSTEM: SOFTWARE: PatentI APPLICATION NUMBER: UPFILING DATE: 19920911 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS ZIP: 61604 COUNTRY: TYPE: AMINO ACID TOPOLOGY: sGlnGlyProPro...... ThrSerPro.....ArgProSerThrSerSer 348 Quality: Peoria I Ratio: 1958 amino acids USA 309-685-4128 linear PatentIn Release #1.0, Version #1.25 Floppy disk 128.00 .0.877 35.351 US/07/945,283 Gaps: 20
Percent Identity: 21.792 304 342

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139	GAGGAGCTGGTGAGCATGAACG	1090
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ο α	GGAAAGTGCAGGTGTCCTCTCAAGGCCCAGGTACATCCTCCCCCCCC	4
	GluAsp	1032
\vdash	:: ::::: ::: rgArgArgAlaGluGlyThrGluAlaAlaAlaAlaAlaAspAlaGluGluGlu 5	w
	ATCGCCAAGTCCCAGGAGCG	_
011	Tysa S	534
	ProGlyArgGlyGlyArgArgGlyGly	N
61	GGAAGTGCGCAAAATCAAACAAGGCCTTGGGCTTGAAATTTGCTGAGCTGG 9 :::	ũ
11 23	roAlaGlyGlySerAlaArgArgArgArgArgGlyGlyGlyGlyGlyPro 5	507
07	OPTOPTOLeuProProProProProProProProProGlnProProp 5	876
75	CCATCCTTTACCA8	റെ
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62	CTTCATTGGAATGAAGTCCCGAGGTATCTACGAGACCCCCAGCAGGCA 8	816
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61	aGlnThrLeuPheSerHisSerGluAsnLysLeuPheSerHisProMe	4-
67		•
44	uAsnThr	421
67		75
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75.7	AACGTCAAGGATGGCACCACCCAGCCAGACCTCCTTGGAGCTCTT	0
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398	HisHisGlnAspProProGlyGlyGlyProProSerProProPro	60
558	CTACACGAAGACCCA	\vdash
517 382	1ProGlyGlyGlyProProSerThrSerSerHisHis 3	37
7	SHISHISGINASPPTO	n d
567	TCACTCCCAAGAACCCGTGGAGCATGGATGAGAACCTCATGCACATCAGC	298 218

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alignment_block:
US-09-775-693-1 x US-08-735-041A-2
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                                                                                                                                                                                                                                                                                                                       Align seg 1/1 to: US-08-735-041A-2 from: 1 to: 539
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPAX: 805.493.... 2:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
SEQUENCE SARACTERISTICS:
SEQUENCE SARACTERISTICS:
SEQUENCE SARACTERISTICS:
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                     227 ......CCATCCAGCGACTC 246
                                                                           217 erProAsnAlaAlaValLeuTrpLeuTrpSerSerHisAsnArgValAsn 233
                                                                                                                   186 GGATGTCAGCAGGAGTTTGTGGAGGAGGTTCATCTGGCCGG..... 226
                                                                                                                                                                                                 136 GAAGCCAGGAAGAAGGCACTGAAGCTTGGGGGCCAAAAAGGTGTTCATTGA 185
                                                                                                                                                                                                                                       185 ProSerHisProArgLeuAlaAlaLeuLeuLeuArgLeuProArgLeuAr 201
                                                                                                                                                         201 gLysProLeuArgAlaAspAlaAlaAlaSerMetHisArgValGly...S 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/735,041A FILING DATE: 22-0CT-1996 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: 805.447.4112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 1840 CITY: Thousand Oaks
STATE: California
                                                                                                                                                                                                                                                                           98 CCTATCTGGCCAACATTGGCC.....AGAAGGAAGACTTCGAG 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 555 ...
TENGTH: 555 ...
TYPE: amino acid
sin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
TOPOLOGY: lin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Mazza, Richard J. REGISTRATION NUMBER: 27,657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Quality:
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1840 De Havilland Drive
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VENTION: PLACENTAL-DERIVED PROSTRATE GROWTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Martin, Francis H.
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0.760
40.732
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Gaps: 26
Percent Identity: 25.366
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	78
SCYSTTPLeuSerProGlyLeuArgArgThrAlaSerGlyAlaLeuTrpA 4	397
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	708
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CACC 65	620 356
<pre>paacccaagaaccaagcgcctccaggtctct 61 </pre>	570 340
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GATCAGGTCCGGTTTGAGCTCAGCTGCTACTCACTGGCCCCCCAGATAAA 419	370 286
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seq_name: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:US-09-190-476B-2
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patent No. 6025204
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-190-476B-2
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                                                                                                                  alignment_block:
US-09-775-693-1 x US-09-190-476B-2
                                                                         Align seg 1/1 to: US-09-190-476B-2 from: 1 to: 539
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 805.499.6751
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 22-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: MAZZA, RICHARD J.
REGISTRATION NUMBER: 27,65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NERAL INFORMATION: Catherine L.
APPLICANT: Farrell, Catherine L.
APPLICANT: Marthin, Francis H.
APPLICANT: Yabkowitz, Rachel
APPLICANT: Yabkowitz, Rachel
PLACENTAL-DERIVED PROSTRATE GROWTH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
COMPUTER: PC-DOS/MS-DOS
COMPUTER: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: A-TELECOMMUNICATION INFORMATION: TELEPHONE: 805.447.4112
STREET: 1840 De HAV.
CITY: Thousand Oaks
STATE: California
                                  98 CCTATCTGGCCAACATTGGCC.....AGAAGGAAGACTTCGAG 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/09/190,476B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Amgen Inc.
STREET: 1840 De Havilland Drive
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Percent Identity: 25.366
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374 CATGCTCATTTAGACATCGAGGCCTTCACCATGGACCGGGAAGTGCGCAA	824 GAATGAAGTCCCGAGGTATCTACGAGACCCCAGCAGCAGCATCCTTTAC	rgser	TGTACCTGA	08 CAACGTCAAGGATGGCACCACCACCAGACCTC :::	CCTGACATTCTCGAGATCGA	20 ACACGAAGACCCCAGGACCCAGCCAAAGCCCCCAAC	7/0 CGAGGCTGGAATCCTGGAGAACCCCAAGAACCAAGCGCCTCCAGGTCTC 	ACTCCCAAGAACCCGTGGAGCATGGATGAGAACCTCATGCACATCAGCT	70 GCAATGACCTGATGGAGTACGCAAAGCAACACGGGATTCCCATCCCGGT ::::: ::::::::::::::::::::	0 GETCATTGCTCCCTGGAGGATGCCTGAATTCTACAACCGGTTCAAC::::::::::	.86AlaThrSerSerTrpThrSerLeuG	rThrSerSerArgproThrSerProGlnT	20 AGCGGGAGGGGCCAAGTATGTGTCCCACGGCGCCCACAGGAAAGGGGA 	2/0 CACCTETETECCAGGCCCTGCATCGCCCCGCAAACAAGTGGAAATCGCC ::::: 266MetCysProCysGlyThrTrpLysProPr	9 SSerGlyHisProValAsnPheValLeuProAlaThrMetAsnAlaTr	AlaArgLeuGlnValProProAlaArgThrProSerSerProArg	nAlaAlaValLeuTrpLeuTrpSerSerHisAsnArgValA	GGAGTTTGTGGAGGAGTTCATCTGGCCGG	. +
GCA	TTA	CATTG 823	ATGGC 786 uTrpA 414	CTTCA 754 LeuHi 397	GTG lnA	· >>	Λ.: Σ::	AG T	Pro	F 6	euGlnL 295	28	GGGAAC	T -	CCT :: laT	.BCACTG 24 ::: .ArgCy 24	ValAsn 23		FCATTGA 185 ::: 3lyS 217

alignment_scores:

NO: 2:
TELECOMMUNICATION TELEPHONE: 805
REGISTRATION NUMBER: REFERENCE/DOCKET NUMBER:
Richard J.
FILING DATE: 12-NO. 013/333 133 CLASSIFICATION: <unknown></unknown>
CURRENT APPLICATION NUMBER: 0
SOFTWARE: Patentin Release #1.
COMPUTER: IBM PC compat
ABLE FORM: YPF: Floppy dis
CITY: Thous
STREET: 1840 De Hav
NUMBER OF SECTION FOR SECTION
FACTOR
Yabkowitz, Rachel
APPLICANT: Farrell, Catheri
Patent No. 6197939
tation 2, App
seq_name: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-09-190-938B-2
521 oCysSerLeuSerGlyLeuGluValTrp 530
CAC
505
CCGTCCTCAAGGGCCAGGTGTACATCCTCGGCCGGGAG
 488 laThrLe
CCACTGCATCGCCAAGTCCCAGGAGCGAGTGGAAGGGAAA
LeuAsnArg
977GGCCTAGCCCTGAGTGTGAATTTGTCCG 1004
455 AspīleSerLeuCysValGlyLeuTyrProCysProSerTrpAlaCysTr 471
953CTGAGCTGGTATACCGGTTTAC 976
441GlyGlnTrpLeuGlnValLeuGlyGlyGlyPheSerTyrLeu 454
924 AATCAAACAAGGCCTTGGAAATTTG952
ThrGlyArg 44
874 CATGCTCATTTAGACATCGAGGCCTTCACCATGGACCGGGAAGTGCGCAA 923
ProAlaGlyGlyProSe
824 GAATGAAGTCCCGAGGTATCTACGAGACCCCAGCAGGCACCATCCTTTAC 873
414 rgSerGlyAlaTrpAlaAlaAlaProSerSerTrpSerThr 427
TGGGCCGTATTGACATCGTGGAGAACCGCTTCATTG

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alignment_block:
US-09-775-693-1 x US-09-190-938B-2
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Ratio: 0.760 Gaps: 26
Percent Similarity: 40.732 Percent Identity: 25.366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Align seg 1/1 to: US-09-190-938B-2 from: 1 to: 539
658 CCTGACATTCTCGAGATCGAGTTCAAAAAAGGGGTCCCTGTGAAGGTGAC 707
                                                              620 ACACGAAGACCCAGGA......CCCAGCCAAAGCCCCCAACACC 657
                                                                                                                                                  340 hr.ProHisvalProAlaGluGlyProGluAlaSerArgProProLysLe 356
                                                                                                                                                                                                570 CGAGGCTGGAATCCTGGAGAACCCCAAGAACCAAGCGCCTCCAGGTCTCT 619
                                                                                                                                                                                                                                       328 yLysProGlu......MetMetLysSerProThrAsnThrT 340
                                                                                                                                                                                                                                                                                   520 ACTCCCAAGAACCCGTGGAGCATGGATGAGAACCTCATGCACATCAGCTA 569
                                                                                                                                                                                                                                                                                                                                312 AlaMetGlyAlaLeuGluLeuGluSerArgAsnSerThrLeuAspProGl 328
                                                                                                                                                                                                                                                                                                                                                                         470 GCAATGACCTGATGGAGTACGCAAAGCAACACGGGATTCCCCATCCCGGTC 519
                                                                                                                                                                                                                                                                                                                                                                                                                                          420 GGTCATTGCTCCCTGGAGGATGCCTGAATTCTACAACCGGTTCAAGGGCC 469
                                                                                                                                                                                                                                                                                                                                                                                                                     286 .....AlaThrSerSerTrpThrSerLeuGlnL 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                370 GATCAGGTCCGGTTTGAGCTCAGCTGCTACTCACTGGCCCCCCAGATAAA 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        276 Ser.....ThrSerSerArgProThrSerProGln..... 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               320 AGCGGAGGGGCCAAGTATGTGTCCCACGGCGCCACAGGAAAGGGGAAC 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             266 ......MetCysProCysGlyThrTrpLysProPro 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       270 CACCTCTCTTGCCAGGCCCTGCATCGCCCGCAAACAAGTGGAAATCGCCC 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 249 sSerGlyHisProValAsnPheValLeuProAlaThrMetAsnAlaTrp. 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             247 TATG.....AGGACCGCTACCTCCTGGG 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       234 AlaArgLeuGlnValProProAlaArgThrProSerSerPro...ArgCy 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                227 .....CCATCCAGTCCAGCCCACTG 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          217 erProAsnAlaAlaValLeuTrpLeuTrpSerSerHisAsnArgValAsn 233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          136 GAAGCCAGGAAGAAGGCACTGAAGCTTGGGGCCCAAAAAGGTGTTCATTGA 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              201 gLysProLeuArgAlaAspAlaAlaAlaSerMetHisArgValGly...S 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    185 ProSerHisProArgLeuAlaAlaLeuLeuLeuArgLeuProArgLeuAr 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98 CCTATCTGGCCAACATTGGCC......AGAAGGAAGACTTCGAG 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 539 amino acids
TYPE: amino acid
STRANDEDNESS: single
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COMPUTER F MEDIUM I	
Houston Texas : UNITED STAT	
CORRESPONDENCE ADDRESS ADDRESSEE: Arnold, STREET: P.O. Box 44	
TITLE OF INVENTION: TITLE OF INVENTION: NUMBER OF SEQUENCES:	
APPLICANT: TELEPHONE NO: (512)4 APPLICANT: TELEPAX: (512)400-4	
APPLICANT: COUNTRY:	
APPLICANT: STREET: APPLICANT: STREET: APPLICANT: CITY:	
<pre>seq_documentation_block: Sequence 2, Application PC/TUS9509; GENERAL INFORMATION: APPLICANT: APPLICANT:</pre>	
<pre>seq_name: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:PCT-US95-09261-2</pre>	
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50	
1005 CCACTGCATGGCAAGTCCCAGGAGCGAGGGGAAGGGGAAAGTGCAGGTGT 1054 ::: :::	
47	
455 AspileSerLeuCysValGlyLeuTyrProCysProSerTrpAlaCysTr 471	
41GlyGlnTrpLeuGlnValLeuGlyGlyGlyPheSerTyrLeu 45	
24 AATCAAACAAGGCCTGGGCTTGAAATTTG	
TCATTTAGACATCGAGGCCTTCACCATGGACCGGGAAGTGCGCAA 92	
428SerLeuArgProAlaGlyGlyProSer 436	
14 rgSerGlyAlaTr	
CysTrpLeuSerProGlyLeuArgA	
82 GluProLeuGlyGlnTrpH	
.TGGCACCACCACCACCACCACCACCACCACCACCACCACCA	

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TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-09261-2
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US-09-775-693-1 x PCT-US95-09261-2
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Ratio: 0.760
Percent Similarity: 40.732
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SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/09261
FILING DATE: CONCURRENTLY HEREWITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: UTFC422P-TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEPHONE: (713) 789-2679
TELEX: 79-0924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: SERTICH, GARY J.
REGISTRATION NUMBER: 34,4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 136 GAAGCCAGGAAGAAGGCACTGAAGCTTGGGGCCCAAAAAGGTGTTCATTGA 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   185 ProSerHisProArgLeuAlaAlaLeuLeuLeuArgLeuProArgLeuAr 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            201 gLysProLeuArgAlaAspAlaAlaAlaSerMetHisArgValGly...S 217
                                                                                                                                                                                                                                                                                                                                                              234 AlaArgLeuGlnValProProAlaArgThrProSerSerPro...ArgCy 249
                                                                                                                                                                                                                                                                                                                                                                                                                                      217 erProAsnAlaAlaValLeuTrpLeuTrpSerSerHisAsnArgValAsn 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       186 GGATGTCAGCAGGAGTTTGTGGAGGAGGTTCATCTGGCCGG...... 226
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98 CCTATCTGGCCAACATTGGCC.....AGAAGGAAGACTTCGAG 135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 01 FILING DATE: 01-AUG-1994
                                                                                                                                                                                                                                                                                         249 sSerGlyHisProValAsnPheValLeuProAlaThiMetAsnAlaTip. 265
                                                                                                                                                                                                                                                                                                                        247 TATG.....AGGACCGCTACCTCCTGGG 269
                                                                                                                                                                              320 AGCGGGAGGGGCCAAGTATGTGTCCCACGGCGCCACAGGAAAGGGGAAC 369
                                                                                                                                                                                                                   270 CACCTCTTGCCAGGCCCTGCATCGCCCGCAAACAAGTGGAAATCGCCC 319
                                                                                                                                          276 Ser......ThrSerSerArgProThrSerProGln....... 285
                                   420 GGTCATTGCTCCCTGGAGGATGCCTGAATTCTACAACCGGTTCAAGGGCC 469
                                                                                                       370 GATCAGGTCCGGTTTGAGCTCAGCTGCTACTCACTGGCCCCCAGATAAA 419
.....AlaThrSerSerTrpThrSerLeuGlnL 295
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5773249 5773249 NFORMATION: NFORMATION: NFORMARI, Franco A. NT: FERRARI, Franco A.
eq_name: /cgnz_b/ptouata/z/tax/57_500000000000000000000000000000000000
ysSerLeuSerGlyLeuGluValTr
CAATGAGGAGCTGG 11
1055 CCGTCCTCAAGGGCCAGGTGTACATCCTCGGCCGGGAGTCC 1099
504
977
sTr 471
 GlyGlnTrpLeuGlnValLeuGlyGlyGlyPheSerTyrLe
A COANCE AND AND AND CONTROL OF THE
74 CATGCTCATTTAGACAT
43
Thr
97 scysTrpLeuSerProGlyLeuArgArgThrAlaSerGlyAlaLa
55 TGT
708 CAACGTCAAGGATGGCACCACCACCAGACCTCCTTGGAGCTCTTCA 754 ::: :::
658 CCTGACATTCTCGAGATCGAGTTCAAAAAAGGGGTCCCTGTGAAGGTGAC 707
620 ACACGAAGACCCAGGA
GAGGCTGGAATCCTGGAGAACCCAAGAACCAAGCGCCTCCAGGTCTCT 6
TA 56
470 GCAATGACCTGATGGAGTACGCAAAGCAACACGGGATTCCCATCCCGGTC 519

oAlaGlyProGly
)5GlySerArgGlyAspProGlyProProGlyAlaGlngly 9 CAGCGGGAGGGGCCAAGTATGTGTCCCACGGCGCCACAGGAAAGGGGA CHILLIII
GCAAACAAGTGGAAATCGC
CTCTCTTGCCAGGCCCTGCATCGCCC 29
TCCAGCGCACTGTA 24
GGAGTTT 20 : .GlyProA 18
GAAGA GlyPr
Align seg 1/1 to: US-08-642-255-73 from: 1 to: 633
alignment_block: US-09-775-693-1 x US-08-642-255-73
alignment_scores: Quality: 126.50 Ratio: 0.904 Percent Similarity: 36.176 Percent Identity: 26.357
NUMBER OF SEQUENCES: 135 CORRESPONDENCE ADDRESS: ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT STREET: 4 Embarcadero Center, Suite 3400 STREET: 4 Embarcadero Center, Suite 3400 STATE: California COUNTRY: USA ZIP: 94:11-4187 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PATENTIN PC COMPATION: COMPUTER: IBM PC COMPATION SOFTWARE: PATENTIN PC POS/MS-DOS CURRENT APPLICATION NUMBER: US/08/642,255 CURRENT APPLICATION NUMBER: US/08/642,255 CLASSIFICATION NUMBER: 20,015 REFERENCE/DOCKET NUMBER: 20,015 REFERENCE/DOCKET NUMBER: A55556-3/BIR TELEPHONE: (415) 494-8770 TELEFAX: 910 277299 FHT UR SEQUENCE CHARACTERISTICS: LENGTH: 633 amino acids STRANDEDNESS: Single TOPOLOGY: linear WOLECULE TYPE: protein
TITLE OF INVENTION: Drotos

1162 GCCACCGGG 1170 431 AlaGlnGly 433
.112 414
A
965 ATACCGGTTTACGGCCTAGCCCTGAGTGTGAATTTGTCCGCCCACTGCATC 1014
-
S
780 GCATGGCGTGGGCCGTATTGACATCGTGGAGAACCGCTTCATTGGAATGA 829 :::
707 CCAACGTCAAGGATGGCACCACCAGCAGACCTCCTTGGAGCT 749
2/6 lyGlySerArgGlyAspProGlyProproGlyAlaGlnGlyProAlaGly 292
GGTCTCTACACGAAGACCCAGGACCCAGCCAAAGCCCCCAACAC
209 ACGAGGCTGGAATCCTGGAGAACCCCAAGAACCAAGCGCCTCCA 612
GlyAlaGinGlyProAlaGlyProGly
GAGAACCTCATGCACATCAGCT
459 CGCAATGACCTGATGGAGTACGCAAAGCAACACGGGATTCCCATCCCGGT 510
::: AlaGlnGlyp
419 AGGTCATTGCTCCCTGGAGGATGCCTGAATTCTACAACCGGTTCAAGGGC 46

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OM of: US-09-775-693-1 to: PIR_68:*
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Database length: 76174552
Search time (sec): 92.790000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query length: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query: US-09-775-693-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Search information block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Database: PIR_68:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 score_list:
                                                                                                                                                                                               pir1:AJSMRC
pir2:JQ0405
pir2:T43481
                                                                                                                                                                                                                                                                                                                                  pir2:G85980
pir1:JN0506
pir2:G82737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pir2:F69034
pir2:E70621
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pir1:AJHURS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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-MODEL-Frame+_n2p.model -DEV-xlp
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-Q-/C972_1/USPT0_spool/US99775693/runat_12022002_124152_1344/app_query.fasta_1.1315
-DE-PIR_68 -QFMT=-Fastan -SUFFIX-rpr -GAPOD=12.000 -GAPEXT=4.000
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-QGAPEXT=7.000 -XGAPOD=10.000 -XGAPEXT=0.500 -FGAPOD=6.000
-GGAPEXT=7.000 -XGAPOD=10.000 -YGAPEXT=0.500 -DELOP-6.000
-DELEXT=7.000 -XGAPOD=10.000 -YGAPEXT=0.500 -DELOP-6.000
-DELEXT=7.000 -START-1 -MATRIX-blosum62 -TRAMS-human40.cd1
-LIST-45 -DOCALIGN=200 -THR_SCORE-pct -THR_MAX-100 -THR_MIN=0
-LIST-45 -MODE-LOCAL -OUTFMT=pfs -NORM-ext -MINLEN=0
-ALIGN=15 -MODE-LOCAL -OUTFMT=pfs -NORM-ext -MINLEN=0
-ALIGN=15 -MODE-LOCAL -OUTFMT=563 -RORM-ext -MINLEN=0
-MAXLEN=2000000000 -USER-US09775693 -RORM-ext -MINLEN=0
-MAXLEN=2000000000 -USER-US09775693 -RORM-ext -MINLEN=0
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A; Residues: 1-24 <RES>
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                                                                      34 yrLeuAlaAsnIleGlyGlnLysGluAspPheGluGluAlaArgLysLys
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pir1:CGHU1B
pir2:E29149
pir2:S50832
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C;Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 18-Jun-1999
C;Accession: A01195; $06104; 156310
C;Accession: A01195; $06104; 156310
R;Bock, H.G.O.; Su, T.S.; O'Brien, W.E.; Beaudet, A.L.
Nucleic Acids Res. 11, 6505-6512, 1983
A;Title: Sequence for human argininosuccinate synthetase cDNA.
A;Reference number: A01195; MUID:84015388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: protein
A; Residues: 148-161 <15A>
R; Jinno, Y.; Nomiyama, H.; Matuo, S.; Shimada, K.; Matsuda, I.; Saheki, T.
R; Jinnerit. Metab. Dis. 8, 157-159, 1985
A; Title: Structure of the 5' end region of the human argininosuccinate synthetase gen
A; Reference number: I56310; MUID:87113889
A; Accession: I56310
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N;Alternate names: citrulline--aspartate ligase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:X01630; NID:g28871; PIDN:CAA25771.1; PID:g28872
R;Isashiki, Y.; Noda, T.; Kobayashi, K.; Sase, M.; Saheki, T.; Titani, K.
Protein Seq. Data Anal. 2, 283-287, 1989
A;Title: Identification of essential arginine residue(s) for Mg-ATP binding of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Reference number: S06104; MUID:89367258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Pathway: urea cycle (Supperfamily: argininosuccinate synthase (Supperfamily: argininosuccinate synthase c;Keywords: arginine biosynthesis; ATP; homotetramer; ligase; urea cycle c;Keywords: arginine bioding #status experimental F;148-161/Region: ATP binding #status experimental F;149,153/Binding site: Mg-ATP (Glu, Arg) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A.Cross-references: GDB:119010; OMIM:215700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:M34903; NID:g179045; PIDN:AAA51782.1; PID:g179047
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US-09-775-693-1 x AJHURS
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                                                                                                                                                                                                                                                                                       Align seg 1/1 to: AJHURS
                         101 ATCTGGCCAACATTGGCCAGAAGGAAGACTTCGAGGAAGCCAGGAAGAAG
                                                                                                                             51 CTCGTGCATCCTCGTGTGGCTGAAGGAACAAGGCTATGACGTCATTGCCT 100
                                                                                                                                                                                                                                  1 ATGTCCAGCAAAGGCTCCGTGGTTCTGGCCTACAGTGGCGGCCTGGACAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               defects in this gene may cause citrullinemia
                                                                        rSerCysIleLeuValTrpLeuLysGluGlnGlyTyrAspValIleAlaT
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                                                                                                             9q34.1-9q34.1
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100.000
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139.50
139.00
138.50
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178.72
164.75
167.45
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Percent Identity: 100.000
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0.0192
0.0293
0.0293
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| proline-rich protein - mouse
| atrophin-1 - human
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1051 GTGTCCGTCCTCAAGGGCCAGGTGTACATCCTCGGCCGGGAGTCCCCCACT 1100
                                                            1001 TCCGCCACTGCATCGCCAAGTCCCAGGAGCGAGTGGAAGGGAAAGTGCAG 1050
                              317 eAlaGluLeuValTyrThrGlyLeuArgProSerProGluCysGluPheV 334
                                                                                                         951 TGCTGAGCTGGTGTATACCGGTTTACGGCCTAGCCCCTGAGTGTGAATTTG 1000
                                                                                                                                                     301 ThrMetAspArgGluValArgLysIleLysGlnGlyLeuGlyLeuLysPh 317
                                                                                                                                                                                    901 ACCATGGACCGGGAAGTGCGCAAAATCAAACAAGGCCTGGGCTTGAAATT 950
                                                                                                                                                                                                                 801 CATCGTGGAGAACCGCTTCATTGGAATGAAGTCCCGAGGTATCTACGAGA 850
                                                                                                                                                                                                                                                                                                                                                                     751 TTCATGTACCTGAACGAAGTCGCGGGCAAGCATGGCGTGGGCCGTATTGA 800
                                                                                                                                                                                                                                                                                                                                                                                                601 CAAGCGCCTCCAGGTCTCTACACGAAGACCCCAGGACCCAGCCAAAGCCCC 650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          201 GlnAlaProProGlyLeuTyrThrLysThrGlnAspProAlaLysAlaPr 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     184 snLeuMetHisIleSerTyrGluAlaGlyIleLeuGluAsnProLysAsn 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  551 ACCTCATGCACATCAGCTACGAGGCTGGAATCCTGGAGAACCCCCAAGAAC 600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               401 CACTGGCCCCCCAGATAAAGGTCATTGCTCCCTGGAGGATGCCTGAATTC 450
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          301 AAACAAGTGGAAATCGCCCAGCGGGGGGGGGGGCCAAGTATGTGTCCCACGG 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84 luAspArgTyrLeuLeuGlyThrSerLeuAlaArgProCysIleAlaArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    251 AGGACCGCTACCTCCTGGGCACCTCTCTTGCCAGGCCCTGCATCGCCCGC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67 uPheValGluGluPheIleTrpProAlaileGlnSerSerAlaLeuTyrG 84
                                                                                                                                                                                                                                              CCCCAGCAGGCACCATCCTTACCATGCTCATTTAGACATCGAGGCCTTC 900
                                                                                                                                                                                                                                                                            sGlyIleProIleProValThrProLysAsnProTrpSerMetAspGluA 184
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C:Superfamily: argininosuccinate synthase C:Keywords: arginine biosynthesis; homotetramer; ligase; urea cycle F:149,153/Binding site: Mg-ATP (Glu, Arg) #status predicted
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C;Comment: This enzyme catalyzes the formation of argininosuccinate from citrulline a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Surh, L.C.; Morris, S.M.; O'Brien, W.E.; Beaudet, A.L. Nucleic Acids Res. 16, 9352, 1988
A;Title: Nucleotide sequence of the cDNA encoding the rat argininosuccinate synthetas A;Reference number: S01440; MUID:89016648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      argininosuccinate synthase (EC 6.3.4.5) - rat
N;Alternate names: citrulline--aspartate ligase
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 18-Jun-1999
C;Accession: S01440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1 to: AJRTRS from: 1 to: 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-412 <SUR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity: 99.029
                     301 AAACAAGTGGAAATCGCCCAGCGGGAGGGGGCCAAGTATGTGTCCCACGG
                                                                                      251 AGGACCGCTACCTGCGTGGGCACCTCTCTTGCCAGGCCCTGCATCGCCCGC 300
                                                                                                                                                                               151 GCACTGAAGCTTGGGGCCAAAAAGGTGTTCATTGAGGATGTCAGCAGGGA 200
                                                                 84 luAspArgTyrLeuLeuGlyThrSerLeuAlaArgProCysIleAlaArg
                                                                                                                                                                                                                                                                                                                                                                            101 ATCTGGCCAACATTGGCCAGAAGGAAGACTTCGAGGAAGCCAGGAAGAAG 150
                                                                                                                                                     67 uPheValGluGluPheIleTrpProAlaValGlnSerSerAlaLeuTyrG 84
                                                                                                                                                                                                                                         51 AlaLeuLysLeuGlyAlaLysLysValPheIleGluAspValSerLysG1 67
                                                                                                                                                                                                                                                                                                                                  34 yrLeuAlaAsnIleGlyGlnLysGluAspPheGluGluAlaArgLysLys
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1151 AGCCAACTGATGCCACCGGGTTCATCAACATCAATTCCCTCAGGCTGAAG 1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51 CTCGTGCATCCTCGTGTGGCTGAAGGAACAAGGCTATGACGTCATTGCCT 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        401 GluTyrHisArgLeuGlnSerLysValThrAlaLys 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               367 uSerLeuTyrAsnGluGluLeuValSerMetAsnValGlnGlyAspTyrG
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Ratio: 5.113
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                         350
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351 CGCCACAGGAAAGGGGAACGATCAGGTCCGGTTTGAGCTCAGCTGCTACT 400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         451 TACAACCGGTTCAAGGGCCGCAATGACCTGATGGAGTACGCAAAGCAACA 500
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                                                                                                                                                                                                                                                                                                                                   1001 TCCGCCACTGCATCGCCAAGTCCCCAGGAGCGAGTGGAAGGGGAAAGTGCAG 1050
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                                                                               1151 AGCCAACTGATGCCACCGGGTTCATCAACATCAATTCCCTCAGGCTGAAG 1200
                                                                                                                                                                1101 GTCTCTCTACAATGAGGAGCTGGTGAGCATGAACGTGCAGGGTGATTATG 1150
                                                                                                                                                                                                                                                1051 GTGTCCGTCCTCAAGGGCCAGGTGTACATCCTCGGCCGGGAGTCCCCCACT 1100
1201 GAATATCATCGTCTCCAGAGCAAGGTCACTGCCAAA 1236
                                                                                                                                                                                                                                                                                                                                                                                                                                                      801 CATCGTGGAGAACCGCTTCATTGGAATGAAGTCCCGAGGTATCTACGAGA 850
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                                                                                                                                                                                                                                                                                                                                                                                                                951 TGCTGAGCTGGTGTATACCGGTTTACGGCCTAGCCCTGAGTGTGAATTTG 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              284
                                                                                                                                                                                                                                                                                       334 alArgHisCysIleAspLysSerGlnGluArgValGluGlyLysValGln 350
                                            384
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAACACCCCTGACATTCTCGAGATCGAGTTCAAAAAAGGGGTCCCTGTGA 700
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                                     284
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GluTyrHisArgLeuGlnSerLysValThrAlaLys 412

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argininosuccinate synthase (EC 6.3.4.5) - mouse N;Alternate names: citrulline--aspartate ligase C.Species: Mus musculus (house mouse) C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 18-Jun-1999 C;Date: 30-Jun-1994 *sequence_revision 30-Jun-1992 #text_change 18-Jun-1999 C;Accession: JU0463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Surh, L.C.; Beaudet, A.L.; O'Brien, W.E. Gene 99, 181-189, 1991
A;Title: Molecular characterization of the murine argininosuccinate synthetase locus A;Reference number: JU0463; MUID:91216457
A;Accession: JU0463.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: mRNA
A;Residues: 1-412 <SUR>
A;Residues: 1-412 <SUR>
A;Cross-references: GB:M31690; NID:g192068; PIDN:AAA37266.1; PID:g309111
C;Comment: This enzyme catalyzes the formation of argininosuccinate from citrulline a C;Cementics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Superfamily: argininosuccinate synthase C;Keywords: arginine biosynthesis; homotetramer; ligase; urea cycle F;149,153/Binding site: Mg-ATP (Glu, Arg) #status predicted
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US-09-775-693-1 x AJMSRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Introns: 35/3; 58/3; 121/3; 142/3; 495/3; 189/2; 199/3; 230/1; 258/2; 280/1; 324/1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             101 ATCTGGCCAACATTGGCCAGAAGGAAGACTTCGAGGAAGCCCAGGAAGAAG 150
                                            251 AGGACCGCTACCTCCTGGGCACCTCTCTTGCCAGGCCCTGCATCGCCCGC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              451 TACAACCGGTTCAAGGGCCGCAATGACCTGATGGAGTACGCAAAGCAACA 500
                                                                                                                                                                                              351 CGCCACAGGAAAGGGGAACGATCAGGTCCGGTTTGAGCTCAGCTGCTACT 400
                                                                                                                                                                                                                                           101 ArgGlnValGluIleAlaGlnArgGluGlyAlaLysTyrValSerHisGl 117
                                                                                                                                                                                                                                                                                             301 AAACAAGIGGAAAICGCCCAGCGGGAGGGGGCCAAGIAIGIGCCCACGG 350
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Percent Identity: 96.117
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argininosuccinate synthase (EC 6.3.4.5) - bovine N.Alternate names: citrulline--aspartate ligase C.Specles: Bos prinigenius taurus (cattle) C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 23-Feb-1997 c.accession: A33986
R;Dennis, J.A.; Healy, P.J.; Beaudet, A.L.; O'Brien, W.E. Proc. Natl. Acad. Sci. U.S.A. 86, 7947-7951, 1989
                                                                                                                                                                             seq_documentation_block:
                                                                                                                                                                                                                             seq_name: pir1:AJBORS
                                                                                                                                                                                                                                                                                             1201 GAATATCATCGTCTCCAGAGCTAGGTCACTGCCAAA 1236
                                                                                                                                                                                                                                                                                                                                                                                                          1151 AGCCAACTGATGCCACCGGGTTCATCAACATCAATTCCCTCAGGCTGAAG 1200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    351 ValSerValPheLysGlyGlnValTyrIleLeuGlyArgGluSerProLe 367
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              217 oAsnSerProAspValLeuGluIleGluPheLysLysGlyValProValL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              651 CAACACCCCTGACATTCTCGAGATCGAGTTCAAAAAAGGGGTCCCTGTGA 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             601 CAAGCGCCTCCAGGTCTCTACACGAAGACCCAGGACCCAGCCAAAGCCCC 650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          551 ACCTCATGCACATCAGCTACGAGGCTGGAATCCTGGAGAACCCCAAGAAC 600
                                                                                                                                                                                                                                                                                                                                                            {\tt luProIleAspAlaThrGlyPheIleAsnIleAsnSerLeuArgLeuLys}
                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTCTCTCTACAATGAGGAGCTGGTGAGCATGAACGTGCAGGGTGATTATG 1150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               {\tt alArgHisCysIleGlnLysSerGlnGluArgValGluGlyLysValGln}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              eAlaGluLeuValTyrThrGlyPheTrpHisSerProGluCysGluPheV 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGCTGAGCTGGTGTATACCGGTTTACCGGCCTAGCCCTGAGTGTGAATTTG 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACCATGGACCGGGAAGTGCGCAAAATCAAACAAGGCCTGGGCTTGAAATT 950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pIleValGluAsnArgPheIleGlyMetLysSerArgGlyIleTyrGluT 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GlnAlaProProGlyLeuTyrThrLysThrGlnAspProAlaLysAlaPr 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sGlylleProlleProValThrProLysSerProTrpSerMetAspGluA 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CGGGATTCCCATCCCGGTCACTCCCAAGAACCCCGTGGAGCATGGATGAGA 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TyrAsnArgPheLysGlyArgAsnAspLeuMetGluTyrAlaLysGlnHi 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              234
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A;Title: Molecular definition of bovine argininosuccinate synthase deficiency.
A;Reference number: A33986; MUID:90046714
A;Recession: A33986
A;Molecula type: mRNA
A;Residues: 1-412 <DEN>
A;Residues: 1-412 <DEN>
A;Cross-references: GB:M26198
C;Comment: This enzyme catalyzes the formation of argininosuccinate from citrulline a C;Superfamily: argininosuccinate synthase
C;Superfamily: arginine biosynthesis; homotetramer; ligase; urea cycle
C;Keywords: arginine biosynthesis; homotetramer; ligase; urea cycle
F;149,153/Binding site: Mg-ATP (Glu, Arg) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Align seg 1/1 to: AJBORS from: 1 to: 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-775-693-1 x AJBORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ratio: 5.039 Percent Similarity: 99.272
184 snLeuMetHisIleSerTyrGluAlaGlyIleLeuGluAsnProLysAsn 200
                                                                                                                                                                                                         167 sGlyIleProValProValThrProLysAsnProTrpSerMetAspGluA 184
                                                                                                                                                                                                                                                                501 CGGGATTCCCATCCCGGTCACTCCCAAGAACCCGTGGAGCATGGATGAGA 550
                                                                                                                                                                                                                                                                                                                                                                    451 TACAACCGGTTCAAGGGCCGCAATGACCTGATGGAGTACGCAAAGCAACA 500
                                                                                                                                                                                                                                                                                                                                                                                                                     134 erLeuAlaProGlnIleLysValIleAlaProTrpArgMetProGluPhe 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                 401 CACTGGCCCCCCAGATAAAGGTCATTGCTCCCTGGAGGATGCCTGAATTC 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         301 AAACAAGTGGAAATCGCCCAGCGGGAGGGGGGCCAAGTATGTGTCCCACGG 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              251 AGGACCGCTACCTCCTGGGCACCTCTCTTGCCAGGCCCTGCATCGCCCGC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          101 ATCTGGCCAACATTGGCCAGAAGGAAGACTTCGAGGAAGCCAGGAAGAAG 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84 luAspArgTyrLeuLeuGlyThrSerLeuAlaArgProCysIleAlaArg 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              151 GCACTGAAGCTTGGGGCCAAAAAGGTGTTCATTGAGGATGTCAGCAGGGA 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67 uPheValGluGluPheIleTrpProAlaIleGlnSerSerAlaLeuTyrG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51 AlaLeuLysLeuGlyAlaLysLysValPheIleGluAspIleSerLysGl 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34 yrLeuAlaAsnIleGlyGlnLysGluAspPheGluGluAlaArgLysLys 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51 CTCGTGCATCCTCGTGTGGCTGAAGGAACAAGGCTATGACGTCATTGCCT 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MetSerGlyLysGlySerValValLeuAlaTyrSerGlyGlyLeuAspTh 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ATGTCCAGCAAAGGCTCCGTGGTTCTGGCCTACAGTGGCGGCCTGGACAC
                                                                                                                                 ACCTCATGCACATCAGCTACGAGGCTGGAATCCTGGAGAACCCCCAAGAAC
                                                                                                                                                                                                                                                                                                                     TyrAsnArgPheGlnGlyArgAsnAspLeuMetGluTyrAlaAsnGluHi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CGCCACAGGAAAGGGGAACGATCAGGTCCGGTTTGAGCTCAGCTGCTACT 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LysGlnValGluIleAlaGlnArgGluGlyAlaLysTyrValSerHisGl 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Quality: 2061.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
                                                                                                                                                                                                                                                                                                                     167
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argininosuccinate synthase - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #text_change 21-Jul-2000
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C;Accession: H72210
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Richardson, D.; Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
                                                                                                                                                                                                   A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome sec A;Reference number: A72200; MUID:99287316 A;Accession: H72210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_name: pir2:H72210
C;Genetics:
A;Gene: TM1780
C;Superfamily: argininosuccinate synthase
                                                                                             A; Experimental source: strain MSB8
                                                                                                                                                                              A; Status: preliminary
                                                                                                                                                                                                                                                                              Nature 399, 323-329, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1001 TCCGCCACTGCATCGCCAAGTCCCAGGAGCGAGTGGAAGGGGAAAGTGCAG 1050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1151 AGCCAACTGATGCCACCGGGTTCATCAACATCAATTCCCTCAGGCTGAAG 1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1101 GTCTCTCTACAATGAGGAGCTGGTGAGCATGAACGTGCAGGGTGATTATG 1150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       334 alArgHisCysIleAlaLysSerGlnGluArgValGluGlyLysValGln 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 951 TGCTGAGCTGGTATACCGGTTTACGGCCTAGCCCTGAGTGTGAATTTG 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 284 hrProAlaGlyThrIleLeuTyrHisAlaHisLeuAspIleGluAlaPhe 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      401 GluTyrHisArgLeuGlnAsnLysValThrAlaLys 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            384 luProValAspAlaThrGlyPheIleAsnIleAsnSerLeuArgLeuLys 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CATCGTGGAGAACCGCTTCATTGGAATGAAGTCCCGAGGTATCTACGAGA 850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACCATGGACCGGGAAGTGCGCAAAATCAAACAAGGCCTGGGCTTGAAATT 950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCCCAGCAGGCACCATCCTTTACCATGCTCATTTAGACATCGAGGCCTTC 900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pIleValGluAsnArgPheIleGlyMetLysSerArgGlyIleTyrGluT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTCATGTACCTGAACGAAGTCGCGGGCAAGCATGGCGTGGGCCGTATTGA 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGGTGACCAACGTCAAGGATGGCACCACCCACCAGACCTCCTTGGAGCTC 750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              eAlaGluLeuValTyrThrGlyPheTrpHisSerProGluCysGluPheV 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAATATCATCGTCTCCAGAGCAAGGTCACTGCCAAA 1236
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alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          110 ACATTGGCCAGAAGGAAGACTTCGAGGAAGCCAGGAAGAAGGCACTGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            210 GGAGTTCATCTGGCCGGCCATCCAGTCCAGCGCACTGTATGAGGACCGCT 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               160 CTTGGGGCCAAAAAGGTGTTCATTGAGGATGTCAGCAGGGAGTTTGTGGA 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          310 GAAATCGCCCAGCGGGAGGGGGCCAAGTATGTGTCCCACGGCGCCCACAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    260 ACCTCCTGGGCACCTCTTGCCAGGCCCTGCATCGCCCGCAAACAAGTG 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10 AAAGGCTCCGTGGTTCTGGCCTACAGTGGCGGCCTGGACACCTCGTGCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    135 roAsnLeuLysValIleSerProTrpLysAspProGluPheLeuAlaLys 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    410 CCCAGATAAAGGTCATTGCTCCCTGGAGGATGCCTGAATTCTACAACCGG 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 118 yLysGlyAsnAspGlnValArgPheGluLeuThrTyrAlaAlaLeuAsnP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               360 AAAGGGGAACGATCAGGTCCGGTTTGAGCTCAGCTGCTACTCACTGGCCC 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             35 snvalGlyGlnLysAspAspPheValAlaIleLysGluLysAlaLeuLys 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18 eLeuLysTrpLeuCysGluLysGlyPheAspValIleAlaTyrValAlaA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60 CCTCGTGTGGCTGAAGGAACAAGGCTATGACGTCATTGCCTATCTGGCCA 109
                                                                                                                                                                                                                                                                                                                                                                                                                           560 ACATCAGCTACGAGGCTGGAATCCTGGAGAACCCCAAGAACCAAGCGCCT 609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           168 olleLysValSerLysLysArgProTyrSerGluAspGluAsnLeuMetH 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         510 CATCCCGGTCACTCCCAAGAACCCGTGGAGCATGGATGAGAACCTCATGC 559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      152 PheLysGlyArgThrAspLeuIleAsnTyrAlaMetGluLysGlyIlePr 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      460 TTCAAGGGCCGCAATGACCTGATGGAGTACGCAAAGCAACACGGGATTCC 509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         68 rAspTyrIlePheThrAlaLeuLeuGlyAsnAlaMetTyrGluGlyArgT 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52 ThrGlyAlaSerLysValTyrValGluAspLeuArgArgGluPheValTh 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   710 ACGTCAAGGATGGCACCACCCACCAGACCTCCTTGGAGCTCTTCATGTAC 759
                                                                                                                                                                                   218 uThrLeuLeuGluIleHisPheGluAsnGlyIleProValLysValValA 235
                                                                                                                                                                                                                                   660 TGACATTCTCGAGATCGAGTTCAAAAAAGGGGTCCCTGTGAAGGTGACCA 709
760 CTGAACGAAGTCGCGGGCAAGCATCGCGTGGGCCGTATTGACATCGTGGA 809
                                                                                        235 snLeuLysAspGlyThrGluLysThrAspProLeuGluLeuPheGluTyr 251
                                                                                                                                                                                                                                                                                GluAspValPheThrTrpThrValSerProLysAspAlaProAspGluG1 218
                                                                                                                                                                                                                                                                                                                                CCAGGTCTCTACACGAAGACCCAGGACCCAGCCAAAGCCCCCAACACCCC 659
                                                                                                                                                                                                                                                                                                                                                                                isIleSerHisGluAlaGlyLysLeuGluAspProAlaHisIleProAsp 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Quality: 1226.50
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82.222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             to: 409
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-alignment_block:
US-09-775-693-1 x T40457
                                                                                                                                                                                                                                                                                                                                                         A;Map position: 2
C;Superfamily: argininosuccinate synthase
                                                                                                                                                                                                                                                                                                  alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                   C;Genetics:
A;Gene: SPDB:SPBC428.05c
                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Experimental source: strain 972h-; cosmid c428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A:Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-410 <LYN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R; Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Baker, S.; Mungall, K. submitted to the EMBL Data Library, November 1998 A; Reference number: Z21931 A; Accession: T40457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             argininosuccinate synthase - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:AL034382; PIDN:CAA22280.1; GSPDB:GN00067; SPDB:SPBC428.05c
                                                                                                    Align seg 1/1 to: T40457 from: 1 to: 410
                                                                                                                                                                                                                            Quality: 1083.00
Ratio: 3.384
Percent Similarity: 81.013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_name: pir2:T40457
1210 CGTCTCCAGAGCAAG 1224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1160 ATGCCACCGGGTTCATCAACATCAATTCCCTCAGGCTGAAGGAATATCAT 1209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1110 CAATGAGGAGCTGGTGAGCATGAACGTGCAGGGTGATTATGAGCCAACTG 1159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1060 CTCAAGGGCCAGGTGTACATCCTCGGCCGGGAGTCCCCACTGTCTCTCTA 1109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1010 GCATCGCCAAGTCCCAGGAGCGAGTGGAAGGGAAAGTGCAGGTGTCCGTC 1059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    401 GlnLeuValLysLys 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  385 spSerLysGlyPheIleAsnIleHisAlaLeuArgLeuLys...ValHis 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          368 rAsnProGluLeuSerSerMetAspValGluGlyGlyPheAspAlaThrA 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      352 TyrLysGlyAsnValMetProValAlaArgTyrSerProTyrSerLeuTy 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   335 laPheArgLysAlaGlnGluAsnValThrGlyLysValThrValSerIle 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             318 ulleTyrAsnGlyPheTrpPheSerProGluMetGluPheLeuLeuAlaA 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          960 GGTGTATACCGGTTTACGGCCTAGCCCTGAGTGTGAATTTGTCCGCCACT 1009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          302 LysGluValMetHisLeuArgAspMetLeuAlaProLysPheAlaGluLe 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          910 CGGGAAGTGCGCAAAATCAAACAAGGCCTGGGCTTGAAATTTGCTGAGCT 959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 285 laThrIleLeuTrpIleAlaHisArgAspLeuGluGlyIleThrMetAsp 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    860 GCACCATCCTTTACCATGCTCATTTAGACATCGAGGCCTTCACCATGGAC 909
                                                                                                                                                                                                                  Percent Identity: 54,430
                                                                                                                                                                                                                                                                    Length:
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323 nGlyGlnPhePheSerProCysThrArgMetLeuLeuAlaAlaAsnAsnV 340

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C;Species: Saccharomyces cerevisiae
C;Date: 30-Jun-1992 #sequence_revision 08-Mar-1996 #text_change 23-Mar-2001
C;Accession: S59291; JQ0779; S61721; S66750; S41983
R;Mannhaupt, G; Vetter, I; Schwarzlose, C; Mitzel, S; Feldmann, H.
submitted to the EMBL Data Library, August 1995
A;Rescription: Analysis of a 26kb region on the left arm of yeast chromosome XV.
A;Reference number: S59285
A;Accession: S59281
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A;Cross-references: EMBL:X91067; NID:9984171; C:; Stalon, V.; Falmagne, P.; Nakamura, R:Palmagne, P.; Nakamura, P.; Stalon, V.; Falmagne, P.; Nakamura, P.; Pid: Falmagne, P.; Nakamura, P.; Nakamura, P.; Pid: Falmagne, P.; Nakamura, P.; Pid: Falmagne, P.; Pid: Falmagne
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N;Alternate names: citrulline--aspartate ligase; protein 01228; protein YOL058w
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A;Molecule type: DNA
A;Residues: 1-26,'AT',29-47,'VL',50-60,'GGLS',65-168,'F',170-315,'L',317-420 <VAN>
A;Residues: 1-26,'AT',29-47,'VL',50-60,'GGLS',65-168,'F',170-315,'L',317-420 <VAN>
A;Residues: 1-26,'AT',184-171, PID:9171085
A;Mannhaupt, G.; Vetter, I.; Schwarzlose, C.; Mitzel, S.; Feldmann, H.
Yeast 12, 67-76, 1996
A;Title: Analysis of a 26 kb region on the left arm of yeast chromosome XV.
A;Reference number: S61713; MUID:96381248
A;Accession: S61721
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A;Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1995
R;Feldmann, H.; Mannhaupt, G.; Vetter, I.
submitted to the Protein Sequence Database, July 1996
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A;Accession: S66750
A;Accession: S66750
A;Cossion: S66750
A;Rocession: S66750
A;Rocession: S66750
A;Rocession: S66750
A;Rocession: S66750
A;Cross-references: EMBL:274800; NID:g1419870; PIDN:CAA99067.1; PID:g1419871; GSPDB:GN00
A;Cross-references: EMBL:274800; NID:g1419870; PIDN:CAA99067.1; PID:g1419871; GSPDB:GN00
A;Cossion: S66750
A;Rocession: S66750
A;Rocession:
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A; Residues: 1-420 <MAN>
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A;Gene: SGD:ARG1; MIPS:YOL058w
A;Cross-references: SGD:S0005419; MIPS:YOL058w
A;Map position: 15L
                                                                                                                                                                                                                                                                                                                                             A;Molecule type: DNA
A;Residues: 1-26,'AT',29-47,'VL',50-57 <CRA>
A;Cross-references: EMBL:X07070; NID:g3371; PIDN:CAA30106.1; PID:g3372
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                           1116 GGAGCTGGTGAGCATGAACGTGCAGGGTGATTATGAGCCAACTGATGCCA 1165
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C;Superfamily: argininosuccinate synthase C;Keywords: arginine biosynthesis; homotetramer; ligase F;148,152/Binding site: Mg-ATP (Glu, Arg) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   157 AAGCTTGGGGCCAAAAAGGTGTTCATTGAGGATGTCAGCAGGGAGTTTGT 206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     357 AGGAAAGGGGAACGATCAGGTCCGGTTTGAGCTCAGCTGCTACTCACTGG 406
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           307 GTGGAAATCGCCCAGCGGGAGGGGGCCAAGTATGTCTCCCACGGCGCCCAC 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    135 ysProAspValLysCysIleThrProTrpArgMetProGluPhePheGlu 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      407 CCCCCCAGATAAAGGTCATTGCTCCCTGGAGGATGCCTGAATTCTACAAC 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52 LysIleGlyAlaCysLysPheValCysValAspCysArgGluAspPheVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35 laAsnValGlyGlnGluGluAspPheAspAlaAlaLysGluLysAlaLeu
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                                                                                                                                                                                                               185 laHisIleSerTyrGluAlaGlyIleLeuGluAspProAspThrThrPro 201
                                                                                                                                                                                                                                                                    557 TGCACATCAGCTACGAGGCTGGAATCCTGGAGAACCCCAAGAACCAAGCG 606
                                                                                                                                                                                                                                                                                                                     168 eProValAlaGlnThrLysAlaLysProTrpSerThrAspGluAsnGlnA 185
                                                                                                                                                                                                                                                                                                                                                                          507 TCCCATCCCGGTCACTCCCAAGAACCCGTGGAGCATGGATGAGAACCTCA 556
                                                                                                                                                                                                                                                                                                                                                                                                                              152 ArgPheAlaGlyArgLysAspLeuLeuAspTyrAlaAlaGlnLysGlyIl 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   457 CGGTTCAAGGGCCGCAATGACCTGATGGAGTACGCAAAGCAACACGGGAT 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       68 lLysAspIleLeuPheProAlaValGlnValAsnAlaValTyrGluAspV 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 AGCAAAGGCTCCGTGGTTCTGGCCTACAGTGGCGGCCTGGACACCTCGTG 56
                                                                                                        202 ProLysAspMetTrpLysLeuIleValAspProMetAspAlaProAspGl 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 SerLysGlyLysValCysLeuAlaTyrSerGlyGlyLeuAspThrSerVa 18
218 nProGlnAspLeuThrIleAspPheGluArgGlyLeuProValLysLeuT 235
                                                     657 CCCTGACATTCTCGAGATCGAGTTCAAAAAAGGGGGTCCCTGTGAAGGTGA 706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rGlyLysGlyAsnAspGlnIleArgPheGluLeuSerPheTyrAlaLeuL 135
                                                                                                                                                           CCTCCAGGTCTCTACACGAAGACCCAGGACCCAGCCAAAGCCCCCAACAC 656
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68

707 CCAACGTCAAGGATGGCACCACCCACCAGACCTCC......TTG 744

US-09-775-693-1 x D75490

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alignment_block:
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C;Acce
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C:Superfamily: argininosuccinate synthase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-402 <WHI>
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                                                                                                Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1042 AAAGTGCAGGTGTCCGTCCTCAAGGGCCAGGTGTACATCCTCGGCCGGGA 1091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             402 IleArgIleLysLysTyrGly......GluSerLysLysThr 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             385 euThrGlyPheLeuProThrAspThrThrGlyPheIleAlaIleGlnAla 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              368 rThrLysThrGluLysLeuTyrAspProThrGluSerSerMetAspGluL 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              352 ThrValArgValArgLeuTyrLysGlyAsnValIleIleLeuGlyArgSe 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               335 ysGluTyrIleArgSerMetIleGlnProSerGlnAsnSerValAsnGly 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               992 GTGAATTTGTCCGCCACTGCATCGCCAAGTCCCAGGAGCGAGTGGAAGGG 1041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    318 rProAsnTyrSerArgLeuIleTyrAsnGlyPheLeuLeuHisProGluC 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    942 CTTGAAATTTGCTGAGCTGGTGTATACCGGTTTACGGCCTAGCCCTGAGT 991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     302 GlyLeuThrLeuAspLysGluValArgGlnLeuArgAspSerPheValTh 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               895 GCCTTCACCATGGACCGGGAAGTGCGCAAAATCAAACAAGGC...CTGGG 941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     285 yrGluGlnAlaProLeuThrValLeuArgLysAlaHisValAspLeuGlu 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          845 ACGAGACCCCAGCAGCACCATCCTTTACCATGCTCATTTAGACATCGAG 894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           268 gIleAspIleValGluAspArgTyrIleAsnLeuLysSerArgGlyCysT 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           795 TATTGACATCGTGGAGAACCGCTTCATTGGAATGAAGTCCCGAGGTATCT 844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           252 AspValPheLeuAlaAlaSerAsnLeuAlaArgAlaAsnGlyValGlyAr 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           745 GAGCTCTTCATGTACCTGAACGAAGTCGCGGGCAAGCATGGCGTGGGCCG 794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           235 hrTyrThrAspAsnLysThrSerLysGluValSerValThrLysProLeu 251
                                                                                                                                                                                           Quality: 1034.00
                                                                                                                                                     Ratio:
                                                                                          76.886
                                                                                                                                                     . 272
                                                                                Percent Identity:
                                                                                                                                                                                     Length:
                                                                50.122
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Align seg 1/1 to: D75490 from: 1 to: 402
854 CAGCAGGCACCATCCTTTACCATGCTCATTTAGACATCGAGGCCTTCACC 903
                                                                                    804 CGTGGAGAACCGCTTCATTGGAATGAAGTCCCGAGGTATCTACGAGACCC 853
                                                      259 uValGluAsnArgPheValGlyMetLysSerArgGlyValTyrGluThrP
                                                                                                                                                                      243 ThrLysAlaAsnGluIleAlaGlyArgHisGlyValGlyArgIleAspLe
                                                                                                                                                                                                                                754 ATGTACCTGAACGAAGTCGCGGGCAAGCATGGCGTGGGCCGTATTGACAT 803
                                                                                                                                                                                                                                                                                    231 leAsnGly......GluGlnLeuSerProAlaAlaLeuLeu 242
                                                                                                                                                                                                                                                                                                                                                                                                    214 rGluAlaGluTyrValGluIleGluTyrValAsnGlyAspProValSerI 231
                                                                                                                                                                                                                                                                                                                                             704 TGACCAACGTCAAGGATGGCACCACCCACCAGACCTCCTTGGAGCTCTTC 753
                                                                                                                                                                                                                                                                                                                                                                                                                                                              654 CACCCCTGACATTCTCGAGATCGAGTTCAAAAAAAGGGGTCCCTGTGAAGG 703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    198 ProProThrHisMetPheLysLeuThrValAsnProGluAspAlaProSe 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           604 GCGCCTCCAGGTCTCTACACGAAGACCCAGGACCCAGCCAAAGCCCCCAA 653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 etLeuHisIleSerTyrGluGlyGlyProLeuGluAspProTrpThrGlu 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        554 TCATGCACATCAGCTACGAGGCTGGAATCCTGGAGAACCCCAAGAACCAA 603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               164 yIleProValProThrThrLysLysAspProTrpSerMetAspAlaAsnM 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     504 GATTCCCATCCCGGTCACTCCCAAGAACCCGTGGAGCATGGATGAGAACC 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               150 .....PheGlnGlyArgAlaAspLeuGluAlaPheAlaArgGluHisGl 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            454 AACCGGTTCAAGGGCCGCAATGACCTGATGGAGTACGCAAAGCAACACGG 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         135 euLysProAspIleValThrValAlaProTrpArgAspTrpAsp..... 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      404 TGGCCCCCAGATAAAGGTCATTGCTCCCTGGAGGATGCCTGAATTCTAC 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          102 MetValGluTleAlaGluLysGluGlyAlaValAlaIleSerHisGlyAl 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             304 CAAGTGGAAATCGCCCAGCGGGAGGGGGCCAAGTATGTGTCCCACGGCGC 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          254 ACCGCTACCTCCTGGGCACCTCTCTTGCCAGGCCCTGCATCGCCCGCAAA 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           204 TGTGGAGGAGTTCATCTGGCCGGCCATCCAGTCCAGCGCACTGTATGAGG 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        154 CTGAAGCTTGGGGCCAAAAAGGTGTTCATTGAGGATGTCAGCAGGGAGTT 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        104 TGGCCAACATTGGCCAGAAGGAAGACTTCGAGGAAGCCAGGAAGAAGGCA 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    85 lyTyrTyrLeuLeuGlyThrSerIleAlaArgProLeuIleAlaLysLys 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    68 eValArgAspTyrValPheProMetMetArgSerSerAlaLeuTyrGluG 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52 LeuAsnThrGlyAlaValAlaAlaTyrAlaLeuAspLeuArgGluGluPh 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  35 hrAlaAspLeuGlyGlnGlyAspGluValGluGluAlaArgValLysAla 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18 eIleLeuLysTrpLeuGlnThrGluArgAsnTyrAspValValCysPheT 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57 CATCCTCGTGTGGCTGAAG...GAACAAGGCTATGACGTCATTGCCTATC 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 SerLysGluLysIleValLeuAlaTyrSerGlyGlyLeuAspThrSerIl 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 AGCAAAGGCTCCGTGGTTCTGGCCTACAGTGGCGGCCTGGACACCTCGTG 56
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A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathd A;Reference number: A82950; MUID:20437337
A;Accession: C83204
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_name: pir2:C83204
                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: DNA
A;Residues: 1-405 <STO>
A;Cross-references: GB:AE004773; GB:AE004091; NID:g9949672; PIDN:AAG06913.1; GSPDB:GN001
                                                                                                                                                                                                                                                                                                                                                              A;Gene: argG; PA3525
C;Superfamily: argininosuccinate synthase
                                                                                                                                                                                                                                                                                                                                                                                                    C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                       A; Experimental source: strain PAO1
                                                                                                                                                                                                                                                                                                       alignment_scores:
                                                                                                                                                                                         alignment_block:
US-09-775-693-1 x C83204
                                                                                                                                                                                                                                          Quality: 927.50
Ratio: 3.011
Percent Similarity: 76.238
                                                                                                                                                Align seg 1/1 to: C83204 from: 1 to: 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1042 AAAGTGCAGGTGTCCGTCCTCAAGGGCCCAGGTGTACATCCTCGGCCGGGA 1091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1192 AGGCTGAAGGAATATCATCGTCTCCAGAGCAAG 1224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1142 GTGATTATGAGCCAACTGATGCCACCGGGTTCATCAACATCAATTCCCTC 1191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1092 GTCCCCACTGTCTCTACAATGAGGAGCTGGTGAGCATGAACGTGCAGG 1141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  954 TGAGCTGGTGTATACCGGTTTACGGCCTAGCCCTGAGTGTGAA...... 996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              904 ATGGACCGGGAAGTGCGCAAAATCAAACAAGGCCTGGGCTTGAAATTTGC 953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  355 salaGluArgSerLeuTyrAspLysAspLeuValSerPhcGluAlaGlyG 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       339 ThralaargLeuLysLeuTyrLysGlyAsnCysIleValAlaGlyArgLy 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  326 lnValTyrPheAspHis...ValAlaLysSer.....ValThrGly 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       997 ....TTTGTCCGCCACTGCATCGCCAAGTCCCAGGAGCGAGTGGAAGGG 1041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  372 lyAspTyrAsnGlnHisAspAlaGlyAlaPheIleLysLeuAsnSerLeu 388
17 rSerValIleLeuLysTrpLeuGlnAspThrTyrAsnCysGluValValT 34
                                  51 CTCGTGCATCCTCGTGTGGCTGAAGGAA...CAAGGCTATGACGTCATTG 97
                                                                       ArgMetArgValGlnLysArgValGluAspLys 399
                      Gaps: 6
Percent Identity: 47.030
                                                                                                                                                                                                                                                                                             Length:
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942 308	892 292	842 275	792 258	742 242	692 230	642 213	592 197	542 - 180	98	48 T	98 A 34 Y	48 C 17 S	98 C	48 A 84 Y	98 G : 57 u	18 AA 11 51 Ly	8 CC
CTTG	GAGG	TCTA ysTy	CCGT	TTGG AlaG	TCCC spll	CAAAG ::: uAsnA	CCCA! ThrT:	TGGAT etAsp	ACACG : sHisG	TCTA :: euLe	CTC# :::	GGCG GlyA	GCAA ::::: YSAI	TGAGG	GAGT:	AGGCA ysAla	CTATC:::
AAAT	CCTT	rglu	ATT(::: Leu/	Ş:: Ω	 □			GA Al	GGAT	AAC ::: Ser	- 0	CCACA	ACAAG ; ;	GACCG :: GlyGl	TTGTG	CTG	TGGC hrAl
TIGC	CACCA: :	35.00 1.00 1.00 1.00 1.00 1.00 1.00 1.00	ACATC	Tec	AGG : :lai	CAAC :::	AAG :: luh	nLe	TCCCA	0 1	Br — CC	GGA Gly	TGGAA :: [leGlu	CTACCTO	GAGG :::: ArgA	a co	CAAC!
TGAGC	TGG! :: euAs	AGC!	GTGG Vale	GTA rGl	: 8	ACCCC ThrPr	<u> </u>	e :: 13	TCC	CAAG uLys	CAGA Gly\	AGGG ysG1	AATCG uIleA	CTCCT	AGTTCA:: :	9 - 9	TTGG :: euGl
TGGT	pAr	GGC/ GLY	AGAA LuAs	CTG!	ACGT	TGAC	CCA Glu	CACATC	Arc	3600	FAAP :: ally	GAACG YASDA	CCCF	eggc	TCT :::	CCAA :: ally	O
STAT	51 E 57	Dr I	Arg	ACG	CAA	ATTO	GTCTC ::: spMet	AGC 	G7 HisG	3CAAT	GGTCAT svalil	ATC!	gcge ::::: nglu	ACCT	ggcc :: yrPi	G:: 🏖	⊢ ≫
ACCGG	GCGC 1A1a	CTTT ::: MetI	TCAT :::: YrVa	AGTC : gval	- W	TCGAG :: leGlu	TACA :::: ETrpL	ACGA yrG1	CACT YLYS	GACC	TTGCT eAla	H — C	GAGGG ThrGl	TCT	GCCA Meti	TGTT::::	
TTTAC	AAAAT :: HisLe	E 2	TGGAAS : :LGlyM	Ē Q	× − C	L D	ACGAA	GGCT ::: uGly	CCCAA LysLy	CTGATG	ICCCT	CGGTT ArgPh	GGC YA1	GCCA AlaA	TCCA ::::	CATT::::Ile	TCG alg
ceecc	rcaaa :: euLys	> G	rgaa etLy	CAAG yIle	ACCC. Lysa	AGTTC ::: hrTyr	GAAGACCC STrpThrA	GGAAT :: GLyVa	AGAAC ::: /sSer	GAGT ::: AspT	GGAG pAr	- >	AGT Sp/	rgPro	GTCCA::::: :::::: :gAlaA	AG Sp	Pr
TAGO	>> · · · C	ATTI isar	GTCC sSer	S ·· A	¥ 5	AAA :::	AGG : las	CCTG : Leu	CCGT		GATGCO gGluT:	GCTCAG	[:: : : :	TGCA Leu]	GCGC :::: snTh	TGTC :::	GCCAG AlaAr
CCTGA	GCCTG uLeu	GAC	rge 	CGTG ::: yIle	ACCT	AAGG ysG1	CCA Pro	GAGAA :: GluAs	GGAGC::: :: yrser	63 29	TGA :: rpas	TGC::::/Ala	TCCC SerH	TCGC	ACTG :::: :rVal	AGCAG ;; ArgGl	9-6
AGT 9	iMe 3	TC 8	C P	GG 7 G1 2	cc 7 ro 2	iGG 69 .yA 23	1 2 C	С 5 Р 1	A 54 M 18	А 49 У 16	A 44 P 15	T 397	A 347 117	C 297	T 247	3 197 1 67	1 50
)91 325	08		41 75	91 58	41 41	30		91	0	3	7	4	7	0 7	7	_	

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alignment_block:
US-09-775-693-1 x C81415
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        argininosuccinate synthase (EC 6.3.4.5) Cj0665c [imported] - Campylobacter jejuni (strai C;Specles: Campylobacter jejuni (;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-May-2000 C;Accession: C81415
R.Parkhill, J; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chillin C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barre Nature 403, 665-668, 2000
A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyphaccession: C81415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Gene: argG; Cj0665c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:AL139075; GB:AL111168; NID:g6967817; PIDN:CAB75297.1; PID:g696812
A;Experimental source: serotype O2, strain NCTC 11168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-406 < PAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Align seg 1/1 to: C81415 from: 1 to: 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_name: pir2:C81415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
                            210 GGAGTTCATCTGGCCGGCCATCCAGTCCAGCGCACTGTATGAGGACCGCT 259
                                                                                                                                                        166 GCCAAAAAG......GTGTTCATTGAGGATGTCAGCAGGGAGTTTGTGGA 209
                                                                                                                                                                                                                                                                   116 GCCAGAAGGAAGACTTCGAGGAAGCCCAGGAAGAAGCACTGAAGCTTGGG 165
74 sAspTyrValPheProMetPheArgAlaAsnAlaIleTyrGluGlyGluT 91
                                                                                                  58 IleLysGluGluAsnIlePheIleLysAspLeuArgAspGluPheValLy 74
                                                                                                                                                                                                           41 lyGlnGlyGluGluLeuGluProAlaArgLysLysAlaLeuSerLeuGly 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1189 CTCAGGCTGAAG 1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1142 GTGAT ...TATGAGCCAACTGATGCCACCGGGTTCATCAACATCAATTCC 1188
                                                                                                                                                                                                                                                                                                                      24 pLeuGlnAspGluTyrAsnCysGluValValThrPheThrAlaAspIleG 41
                                                                                                                                                                                                                                                                                                                                                                      69 GCTGAAG...GAACAAGGCTATGACGTCATTGCCTATCTGGCCAACATTG 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1092 GTCCCCACTGTCTCTCTACAATGAGGAGCTGGTGAGCATGAACGTGCAGG 1141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1042 AAAGTGCAGGTGTCCGTCCTCAAGGGCCAGGTGTACATCCTCGGCCGGGA 1091
                                                                                                                                                                                                                                                                                                                                                                                                                                                          19 GTGGTTCTGGCCTACAGTGGCGGCCTGGACACCTCGTGCATCCTCGTGTG 68
                                                                                                                                                                                                                                                                                                                                                                                                                        8 ValValLeuAlaTyrSerGlyGlyLeuAspThrSerIleIleLeuLysTr 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         392 LeuArgMetArg 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      375 lyGlyAlaTyrAsnGlnAlaAspAlaAlaGlyPheIleLysLeuAsnAla 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            358 sSerAspAspSerLeuPheAspAlaAsnIleAlaThrPheGluGluAspG 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 342 ValValArgLeuLysLeuTyrLysGlyAsnValValValValGlyArgLy 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          325 rgLeuMetLeuGlnGlnMetIleAspAlaSerGlnValAsnValAsnGly 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 892.00
3.014
74.559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    :
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GCCACAGG	1154 CAACTGATGCCACCGGGTTCATCAACATCAATTCCCTCAGG 1194	.04 TCTCTACAATGAGGAGCTGGTGAGCATGAACGTGCAGGGTGATTATGAG ::: 	.057 GTCCTCAAGGGCCAGGTGTACATCCTCGGCCGGGAGTCCCCACTGT ::: ::: 349 LeuTyrLysGlyAsnValMetValIleGlyArgGluSerAlaAsnAspS)7 ACTGCATCGCCAAGTCCCAGGAGGGAGGGAAAGTGCAGGTGTC	957 GCTGGTGTATACCGGTTTACGGCCTAGCCCTGAGTGTGAATTTGTCCGC	07 GACCGGGAAGTGCGCAAAATCAAACAAGGCCTGGGCTTGAAATTTGCTG ::: ::: :: 9 AspArgGluAlaAlaHisLeuLysAspGluLeuMetProLysTyrAlaS	STANDARD STANDARD	07 GGAGAACCGCTTCATTGGAATGAAGTCCCGAGGTATCTACGAGACCCC :::::	'3/ IACUTGAACGAAGTCGCGGGCAAGCATGGCGTGGGCCGTATTGACATCG :::::: ::: :::	'07 CCAACGTCAAGGATGGCACCACCACCAGACCTCCTTGGAGCTCTTCA ::::::::::::::::::::::::::::::::)5/ CCCTGACATTCTCGAGATCGAGTTCAAAAAAAGGGGTCCCTGTGAAGGTG ::: ::: :::: ::: :	0/ CCTCCAGGTCTCTACACGAAGACCCAGGACCCAGACCCAAAGCCCCAACACA 04 GluGluAspMetTrpArgTrpSerLysSerProLysAspAlaProAsnG	ST TGCACATCAGCTACGAGGCTGGAATCCTGGAGAACCCAAGAACCAAGC 	.10 CATCCCGGTCACTCCCAAGAACCCGTGGAGCATGGATGAGAACCT 	60 TTCAAGGGCCGCAATGACCTGATGGAGTACGCAAAGCAACACGGGATT	10 CCCAGATAAAGGTCATTGCTCCCTGGAGGATGCCTGAATTCTACAACC	60 AAAGGGGAACGATCAGGTCCGGTTTGAGCTCAGCTGCTACTCACTGGC 	10 GAAATCGCCCAGCGGGAGGGGGCCAAGTATGTGTCCCACGGGGGCCACA 	
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R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Reference number: A83650; MUID:20263314
A;Accession: C84048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 08-Dec-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                argininosuccinate synthase (citrulline-asparate ligase) argG [imported] - Bacillus halod
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-409 <STO>
A;Cross-references: GB:AP001518; GB:BA000004; NID:g10175792; PIDN:BAB06906.1; GSPDB:GN00
A;Experimental source: strain C-125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_name: pir2:C84048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Gene: argG
C;Superfamily: argininosuccinate synthase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ratio: 2.912
Percent Similarity: 72.439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Align seg 1/1 to: C84048 from: 1 to: 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US^{-}09-775-693-1 \times C84048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           157 AAGCTTGGGGCCAAAAAGGTGTTCATTGAGGATGTCAGCAGGGAGTTTGT 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  107 CCAACATTGGCCAGAAGGAAGACTTCGAGGAAGCCAGGAAGAAGGCACTG 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                207 GGAGGAGTTCATCTGGCCGGCCATCCAGTCCAGCGCACTGTATGAGGACC 256
                                                                                                                                                                                                                                                                        102 ValGluTleAlaGluGlnThrGlyAlaGlnAlaValAlaHisGlyCysTh 118
                                                                                                                                                                                                                                                                                                                         307 GTGGAAATCGCCCAGCGGGAGGGGGCCAAGTATGTGTCCCACGGCGCCCAC 356
                                                                                                                                                                                                                                                                                                                                                                                                                           257 GCTACCTCCTGGGCACCTCTCTTGCCAGGCCCTGCATCGCCCGCAAACAA 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52 LysvalGlyAlaIleGluSerTyrThrIleAspAlaLysLysGluPheAl 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35 euAspValGlyGluGlyLysAspLeuGluPheValLysGluLysAlaLeu 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18 lalaileLysTrpLeuSerAspLysGlyTyrAspValIleAlaValGlyL 35
                                                                                                                     407 CCCCCCAGATAAAGGTCATTGCTCCCTGGAGGATGCCTGAATTCTACAAC 456
                                                                                                                                                                                                                       357 AGGAAAGGGGAACGATCAGGTCCGGTTTGAGCTCAGCTGCTACTCACTGG 406
                                                                    135 snProAsnLeuGluValLeuAlaProValArgGluTrpAlaTrp..... 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 AGCAAAGGCTCCCTGGTTCTGGCCTACAGTGGCGGCCTGGACACCTCGTG 56
                                                                                                                                                                                                                                                                                                                                                                          85 ysTyrProLeuValSerAlaLeuSerArgProLeuIleSerLysLysLeu 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CATCCTCGTGTGGCTGAAGGAACAAGGCTATGACGTCATTGCCTATCTGG 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               aGluGluPheValLeuProAlaLeuGlnAlaHisAlaLeuTyrGluGlnL 85
             CGGTTCAAGGGCCGCAATGACCTGATGGAGTACGCAAAGCAACACGGGAT 506
                                                                                                                                                                      rGlyLysGlyAsnAspGlnValArgPheGluValSerTleGlnAlaLeuA 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Quality:
Ratio:
865.00
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163 eProIleProIleAspLeuAspAsnProTyrSerValAspGlnAsnLeuT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 507 TCCCATCCCGGTCACTCCCAAGAACCCGTGGAGCATGGATGAGAACCTCA 556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   150 .....SerArgAspGluGluIleGluTyrAlaLysLysAsnAsnIl 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          180 rpGlyArgSerAsnGluCysGlyIleLeuGluAspProTrpAlaThrPro 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               557 TGCACATCAGCTACGAGGCTGGAATCCTGGAGAACCCCAAGAACCAAGCG 606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |||:::|||:::||||| :::
213 nproGluIleValGluIleGlyPheGluLySGlyIleProValThrLeu. 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     197 proGluGlyAlaTyrGluLeuThrValAlaIleGluAspAlaProAspGl 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   657 CCCTGACATTCTCGAGATCGAGTTCAAAAAAGGGGTCCCTGTGAAGGTGA 706
                                                                                                                                                                                                                                                                                                                                                          1057 GTCCTCAAGGGCCAGGTGTACATCCTCGGCCGGGAGTCCCCACTGTCTCT 1106
                                                                                                                                                                                                                                                                                                                                                                                                                                                               1007 ACTGCATCGCCAAGTCCCAGGAGCGAGTGGAAAGTGCAAGTGTCC 1056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            757 TACCTGAACGAAGTCGCGGGCAAGCATGGCGTGGGCCGTATTGACATCGT 806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  230 ..AsnGlyLysSerTyrProValHis......GluLeuIleLeu 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                707 CCAACGTCAAGGATGGCACCCACCAGACCTCCTTGGAGCTCTTCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             807 GGAGAACCGCTTCATTGGAATGAAGTCCCGAGGTATCTACGAGACCCCAG 856
                                                                                                                                                                                                                                                         1107 CTACAATGAGGAGCTGGTGAGCATGAACGTGCAGGGTGATTATGAGCCAA 1156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  907 GACCGGGAAGTGCGCAAAATCAAACAAGGCCTGGGCTTGAAATTTGCTGA 956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      275 lyAlaMetThrLeuIleLysAlaHisLysGluLeuGluAspLeuThrLeu 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        857 CAGGCACCATCCTTTACCATGCTCATTTAGACATCGAGGCCTTCACCATG 906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         258 iGluAsnArgLeuValGlyIleLysSerArgGluValTyrGluCysProG 275
                                                                                                                                                    1157 CTGATGCCACCGGGTTCATCAACATCAATTCCCTCAGGCTGAAGGAATAT 1206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 308 uLeuIleTyrGluGlyLeuTrpPheSerProLeuGlnProAlaLeuSerA 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 292 ThrLysGluValAlaHisPheLysProValValGluLysLysIleAlaGl 308
                                                 1207 CATCGTCTCCAGAGCAAGGTCACTGCCAAA 1236
                                                                                                                                                                                                                                                                                                           342 LeuPheLysGiyHisAlaIleValGluGlyArgLysSerGluTyrSerLe 358
                                                                                                                                                                                                                                                                                                                                                                                                           325 lapheLeuLysGluThrGinSerThrValThrGlyValValArgValLys 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  957 GCTGGTGTATACCGGTTTTACGGCCTAGCCCTGAGTGTGAATTTGTCCGCC 1006
                                                                                                                                                                                                        358 uTyrAsnGluLysLeuAlaThrTyrThrProAspAspGluPheAspHisA 375
                                                                                                     375 snAlaAlaValGlyPheIleSerLeuTrpGlyLeuProThrLysValTyr 391
392 SerMetValAsnLysGluMetLysGluLys 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCTCCAGGTCTCTACACGAAGACCCAGGGACCCAGCCAAAGCCCCCCAACAC 656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               756
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R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bei C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, Nature 390, 249-256, 1997

C;Species: Bacillus subtilis C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000

argininosuccinate synthase argG - Bacillus subtilis

seq_name: pir2:B69589

seq_documentation_block:

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alignment_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Superfamily: argininosuccinate synthase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-403 <KUN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Gene: argG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:Z99118; GB:Z99119; GB:AL009126; NID:g2635411; PIDN:CAB14923.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to: B69589 from: 1 to: 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-775-693-1 x B69589
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
151 .....SerArgGluGluGluIleGluTyrAlaAlaSerAr 162
                                                                                                                                                                                                                                             401 CACTGGCCCCCAGATAAAGGTCATTGCTCCCTGGAGGATGCCTGAATTC 450
                                                                                   451 TACAACCGGTTCAAGGGCCGCAATGACCTGATGGAGTACGCAAAGCAACA 500
                                                                                                                                                              134 erLeuAsnProAspLeuGluValIleAlaProValArgGluTrpGlnTrp 150
                                                                                                                                                                                                                                                                                                                                117 yCysThrGlyLysGlyAsnAspGlnValArgPheGluValSerIleLysS 134
                                                                                                                                                                                                                                                                                                                                                                                                           351 CGCCACAGGAAAGGGGAACGATCAGGTCCGGTTTGAGCTCAGCTGCTACT 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          101 LysLeuValGluileAlaGluLysGluAspAlaGlnAlaIleAlaHisGl 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             301 AAACAAGTGGAAATCGCCCAGCGGGAGGGGGCCAAGTATGTGTCCCACGG 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       251 AGGACCGCTACCTCCTGGGCACCTCTCTTGCCAGGCCCTGCATCGCCCGC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         151 GCACTGAAGCTTGGGGCCAAAAAGGTGTTCATTGAGGATGTCAGCAGGGA 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84 luGlyLysTyrProLeuValSerAlaLeuSerArgProLeuIleAlaLys 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     101 ATCTGGCCAACATTGGCCAGAAGGAAGACTTCGAGGAAGCCAGGAAGAAG 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51 AlaLeuGluValGlyAlaThrAsnSerTyrValIleAspAlaLysGluGl 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34 ysCysLeuAspValGlyGluGlyLysAspLeuAlaPheValGlnGlnLys 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51 CTCGTGCATCCTCGTGTGGCTGAAGGAACAAGGCTATGACGTCATTGCCT 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ATGTCCAGCAAAGGCTCCGTGGTTCTGGCCTACAGTGGCGGCCTGGACAC 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          uPheAlaGlnAspTyrAlaLeuIleSerLeuGlnAlaHisThrMetTyrG 84 \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ratio:
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2.773
73.750
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A;Cross-references: EMBL:AL049657; GSPDB:GN00062; ATSP:F617.40 A;Experimental source: cultivar Columbia; BAC clone F617

A;Reference number: Z15792 A;Accession: T06667 A;Molecule type: DNA A;Residues: 1-498 <BEV>

R:Bevan, M.; Terryn, N.; Ardiles, W.; Buysshaert, C.; Dasseville, R.; De Clerck, R.; submitted to the Protein Sequence Database, April 1999

argininosuccinate synthase (EC 6.3.4.5) - Arabidopsis thaliana N;Alternate names: protein F677.40 C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 22-Oct-1999 C;Accession: T06667

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seq_documentation_block:
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                                                                                                                                1151 AGCCAACTGATGCCACCGGGTTCATCAACATCAATTCCCTCAGGCTGAAG 1200
                                                                                                                                                                                                                                    1101 GTCTCTCTACAATGAGGAGCTGGTGAGCATGAACGTGCAGGGTGATTATG 1150
                                                                                                                                                                                                                                                                                                                                        1051 GTGTCCGTCCTGAAGGGCCAGGTGTACATCCTCGGCCGGGAGTCCCCACT 1100
                                                                                374 spHisHisAlaAlaIleGlyPheIleGluLeuTrpGlyLeuProThrLys 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                1001 TCCGCCACTGCATCGCCAAGTCCCAGGAGCGAGTGGAAAGGGGAAAGTGCAG 1050
                                                                                                                                                                                  357 rSerLeuTyrAspGluLysLeuAlaThrTyrThrLysAspAspAlaPheA 374
                                                                                                                                                                                                                                                                                         341 ValLysLeuPhcLysGlyHisAlaIleValGluGlyArgLysSerGluTy 357
                                                                                                                                                                                                                                                                                                                                                                                             324 euHisAlaPheLeuLysGluThrGlnLysHisValThrGlyIleValArg 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  307 tSerGluIleIleTyrAsnGlyLeuTrpPheSerProLeuLysAspAlaL 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 951 TGCTGAGCTGGTGTATACCGGTTTACGGCCTAGCCCTGAGTGTGAATTTG 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      291 ThrLeuValLysGluValAlaHisPheLysProIleIleGluGlnLysMe 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        901 ACCATGGACCGGGAAGTGCGCAAAATCAAACAAGGCCTGGGCTTGAAATT 950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        274 ysProGlyAlaMetThrLeuIleLysAlaHisLysGluLeuGluAspLeu 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               851 CCCCAGCAGGCACCATCCTTTACCATGCTCATTTAGACATCGAGGCCTTC 900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 801 CATCGTGGAGAACCGCTTCATTGGAATGAAGTCCCGAGGTATCTACGAGA 850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 IleLeuLysLeuAsnGluMetAlaGlyAlaHisGlyValGlyArgIleAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     751 TTCATGTACCTGAACGAAGTCGCGGGCAAGCATGGCGTGGGCCGTATTGA 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     229 erIle......AspGlyValSerTyrSerLeuSer...GluLeu 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            701 AGGTGACCAACGTCAAGGATGGCACCACCACCAGACCTCCTTGGAGCTC 750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            212 oAspThrProGluValIleGluIleAlaPheGluGlnGlyValProValS 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 651 CAACACCCCTGACATTCTCGAGATCGAGTTCAAAAAAAGGGGTCCCTGTGA 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   196 AlaProProGluGlyAlaTyrAspLeuThrAlaProLeuGluLysThrPr 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     601 CAAGCGCCTCCAGGTCTCTACACGAAGACCCAGGACCCAGGCCAAAGCCCC 650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          551 ACCTCATGCACATCAGCTACGAGGCTGGAATCCTGGAGAACCCCAAGAAC 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            162 gGlyTleProTleProTleAsnLeuAspSerProTyrSerTleAspGlnA 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        501 CGGGATTCCCATCCCGGTCACTCCCAAGAACCCCGTGGAGCATGGATGAGA 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PHisValGluAsnArgLeuValGlyIleLysSerArgGluValTyrGluC 274
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A;Map position: 4
A;Introns: 25/1; 100/1; 146/2; 162/3; 223/3; 285/3; 315/2
C;Superfamily: argininosuccinate synthase
C;Keywords: ligase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Gene: ATSP: F617.40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_block:
US-09-775-693-1 x T06667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         161 lyGlnGlyIleLysGluLeuGluGlyLeuGluGlnLysAlaLysAlaSer 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             116 GCCAGAAG...GAAGACTTCGAGGAAGCCAGGAAGAAGCACTGAAGCTT 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    178 GlyAlaSerGlnLeuValValLysAspLeuThrGluGluPheValLysAs 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          163 GGGGCCAAAAAGGTGTTCATTGAGGATGTCAGCAGGGAGTTTGTGGAGGA 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         213 GTTCATCTGGCCGGCCATCCAGTCCAGCGCACTGTATGAGGACCGCTACC 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19 GTGGTTCTGGCCTACAGTGGCGGCCTGGACACCTCGTGCATCCTCGTGTG 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             263 TCCTGGGCACCTCTTGCCAGGCCCTGCATCGCCCGCAAACAAGTGGAA 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             194 pPhellePheProCysLeuArgAlaGlyAlaIleTyrGluArgLysTyrL 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              69 GCTGAAGGAACAA...GGCTATGACGTCATTGCCTATCTGGCCAACATTG 115
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                                                                                                                                                                                                                                                                                                                                                                                                                                   236 luLeuLysValValAlaProTrpArgGluTrpGlu......Ile 248
                                                                                                                                                                                                                                                                                                                                                                                        463 AAGGGCCGCAATGACCTGATGGAGTACGCAAAGCAACACGGGGATTCCCAT 512
                                                                                                                                                                                                                                                                                                                                              249 GlnGlyArgGluAspAlaIleGluTyrAlaLysLysHisAsnValProVa 265
                                                                                                                            613 GGTCTCTACACGAAGACCCAGGACCCAGCCCAAAGCCCCCAACACCCCCTGA 662
                                                                                                                                                                      ::|||:::|||::: :::||||||:::||| | |||:::
282 euSerHisGluGlyAspLeuLeuGluAspProAlaAsnGluProLysLys 298
                                                                                                                                                                                                               563 TCAGCTACGAGGCTGGAATCCTGGAGAACCCCAAGAACCAAGCGCCTCCA 612
                                                                                                                                                                                                                                                           265 lprovalThrLysLysSerIleTyrSerArgAspArgAsnLeuTrpHisL 282
                                                                                                                                                                                                                                                                                                  513 CCCGGTCACTCCCAAGAACCCGTGGAGCATGGATGAGAACCTCATGCACA 562
                                                                                   299 AspMetTyrMetMetSerValAspProGluAspAlaProAspGlnProGl 315
315 uTyrIleGluIleGlyIleGluSerGlyLeuProValAlaLeuAsnGly. 331
                                           663 CATTCTCGAGATCGAGTTCAAAAAAGGGGTCCCTGTGAAGGTGACCAACG 712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .....valArgPheGluLeuThrPhePheSerLeuAsnProG 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Quality:
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2.890
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seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_name: pir2:E84935
                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Accession: E84935
R;Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Tshikawa, H.
Nature 407, 81-86, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Buchnera sp.
C;Date: 02-mar-2001 #sequence_revision 02-mar-2001 #text_change 23-Mar-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            argininosuccinate synthase (BC 6.3.4.5) [imported] - Buchnera sp. (strain APS)
                                                                                                                                                                                                                                                                                                                                                                                                  A; Reference number: A84930; MUID:20445173
A; Accession: E84935
                                                                                                                                                                                                                                      C; Superfamily: argininosuccinate synthase
                                                                                                                                                                                                                                                                                                A; Experimental source: strain APS
                                                                                                                                                                                                                                                                                                                   A; Cross-references: GB: AP000398; GSPDB: GN00144
                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-403 <STO>
                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                      A, Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp
                                                                                                                                                                                                                       C; Keywords: ligase
                                                                                                                                                                                                                                                         A;Gene: argG; BU050
                                                                                                                                                                                                                                                                                 C; Genetics:
                                                                                                                                                           alignment_scores:
                                          alignment_block:
US-09-775-693-1 x E84935
Align seg 1/1 to: E84935 from: 1 to: 403
                                                                                                    Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             332 .....LysalaLeuSerProAlaThrLeuLeuAlaGluLeu 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           763 AACGAAGTCGCGGGCAAGCATGGCGTGGGCCGTATTGACATCGTGGAGAA 812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        713 TCAAGGATGGCACCACCCACACACCTCCTTGGAGCTCTTCATGTACCTG 762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        813 CCGCTTCATTGGAATGAAGTCCCGAGGTATCTACGAGACCCCAGCAGGCA 862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                344 AsnThrIleGlyGlyLysHisGlyIleGlyArglleAspMetValGluAs 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1063 AAGGGCCAGGTGTACATCCTCGGCCGGGAGTCCCCACTGTCTCTCTACAA 1112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           913 GAAGTGCGCAAAATCAAACAAGGCCTGGGCTTGAAATTTGCTGAGCTGGT 962
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 863 CCATCCTTTACCATGCTCATTTAGACATCGAGGCCTTCACCATGGACCGG 912
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394 GluSerIleGlnValLysAspThrLeuAlaLeuLysTyrAlaGluMetVa 410
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444 LysGlySerValSerValThrGlyArgGlnSerProAsnSerLeuTyrAr 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              460 gGlnAspIleSerSerPheGluGlySerGluIleTyrAsnGlnAlaAspA 477
                                                                                                                                               Quality:
                                                                                                          807.50
2.710
75.253
                                                                                                            Percent Identity: 43.687
                                                                                                                                                         Length:
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283 hrileileMetThrAlaileLysAlaileGluGlnLeuValLeuAspArg 299
                                      863 CCATCCTTTACCATGCTCATTTAGACATCGAGGCCTTCACCATGGACCGG 912
                                                                                                  813 CCGCTTCATTGGAATGAAGTCCCGAGGTATCTACGAGACCCCAGCAGGCA 862
                                                                          266 nArgLeuileGlyMetLysSerArgGlyCysTyrGluThrProGlyGlyT 283
                                                                                                                                                         250 AsnSerLeuGlyAlaLysHisGlyIleGlyArgIleAspIleIleGluAs 266
                                                                                                                                                                                                763 AACGAAGTCGCGGGCAAGCATGGCGTGGGCCGTATTGACATCGTGGAGAA 812
                                                                                                                                                                                                                                      238 lnLys.....LeuAsnProLeuLysCysValGluGluLeu 249
                                                                                                                                                                                                                                                                               713 TCAAGGATGGCACCACCACCAGACCTCCTTGGAGCTCTTCATGTACCTG 762
                                                                                                                                                                                                                                                                                                                   663 CATTCTCGAGATCGAGTTCAAAAAAGGGGTCCCTGTGAAGGTGACCAACG 712
                                                                                                                                                                                                                                                                                                                                                                                                  205 ASPCysTrpSerTrpThrValAsnProGluAspAlaProGluLysProGl 221
                                                                                                                                                                                                                                                                                                                                                                                                                                         613 GGTCTCTACACGAAGACCCCAGGACCCAGCCAAAGCCCCCAACACCCCCTGA 662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           188 leSerThrGluGlyGlyLeuLeuGluAsnProTrpAsnGlnSerAsnGlu 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     563 TCAGCTACGAGGCTGGAATCCTGGAGAACCCCAAGAACCAAGCGCCTCCA 612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        171 rThrAiaThrLeuGluLysIleTyrSerLysAspGluAsnSerTrpHisI 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                513 CCCGGTCACTCCCAAGAACCCGTGGAGGCATGGATGAGAACCTCATGCACA 562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     155 AsnSerArgGluSerLeuLeuLysTyrLeuAspLysLysAsnIleSerTh 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             463 AAGGGCCGCAATGACCTGATGGAGTACGCAAAGCAACACGGGGATTCCCCAT 512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           142 snLeuAsnVallleAlaProTrpArg.....GluTrp.....AsnLeu 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               413 AGATAAAGGTCATTGCTCCCTGGAGGATGCCTGAATTCTACAACCGGTTC 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            109 LeuAlaLeuAsnIleGlyAlaAsnSerLeuCysHisGlyAlaThrGlyLy 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  313 ATCGCCCAGCGGGAGGGGGCCAAGTATGTGTCCCACGGGGCCCACAGGAAA 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                263 TCCTGGGCACCTCTCTTGCCAGGCCCTGCATCGCCCGCAAACAAGTGGAA 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            213 GTTCATCTGGCCGGCCATCCAGTCCAGCGCACTGTATGAGGACCGCTACC 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         163 GGGGCCAAAAAGGTGTTCATTGAGGATGTCAGCAGGGAGTTTGTGGAGGA 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92 euLeuGlyThrAlaMetAlaArgProIleIleAlaLysLysGlnValGlu 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   75 nTyrValTyrProValLeuLysThrGlyAlaLeuTyrGluGlySerTyrL 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    116 GCCAG...AAGGAAGACTTCGAGGAAGCCAGGAAGAAGGCACTGAAGCTT 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59 GlyAlaSerSerCysHisValPheAspLeuLysGluGluPheIleGluAs 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42 lyGlnSerLysLysAspLeuAsnGlyIleGluLysLysSerLeuGluSer 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25 pLeuLysGluAsnTyrAsnPheGluValValAlaPheValAlaAspIleG 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                69 GCTGAAGGAACAA...GGCTATGACGTCATTGCCTATCTGGCCAACATTG 115
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alignment_block:
US-09-775-693-1 x B70398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GB:AE000725; NID:g2983598; PIDN:AAC07170.1; PID:g2983600; GB:AE00A;Experimental source: strain VF5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Gene:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-401 <AQF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                  Align seg 1/1 to: B70398 from: 1 to: 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus. A:Reference number: A70300; MUID:98196666 A:Accession: B70398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity: 72.277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 392, 353-358, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          argininosuccinate synthase - Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 16-Jul-1999
C;Accession: B70398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_documentation_block;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_name: pir2:B70398
                                          160 CTTGGGGCCAAAAAGGTGTTCATTGAGGATGTCAGCAGGGAGTTTGTGGA 209
                                                                                                                                110 ACATTGGCCAGAAGGAAGACTTCGAGGAAGCCAGGAAGAAGACGCACTGAAG 159
53 AlaGlyAlaIleGluAlaIleValGluAspLeuLysGluThrPheAlaGl 69
                                                                                        36 spValGlyGlnGlyGluGluLeuSerGluIleProGluLysAlaArgArg 52
                                                                                                                                                                             19 eValArgTrpLeuThrGluLysGlyTyrGluValIIeThrTyrThrAlaA 36
                                                                                                                                                                                                                   60 CCTCGTGTGGCTGAAGGAACAAGGCTATGACGTCATTGCCTATCTGGCCA 109
                                                                                                                                                                                                                                                                                                              10 AAAGGCTCCGTGGTTCTGGCCTACAGTGGCGGCCTGGACACCTCGTGCAT 59
                                                                                                                                                                                                                                                                 1163 CCACCGGGTTCATCAACATCAATTCCCTCAGGCTGAAG 1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1113 TGAGGAGCTGGTGAGCATGAACGTGCAGGGTGATTATGAGCCAACTGATG 1162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              383 laAspGlyPheIleArgLeuPheSerLeuSerSerLys 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1063 AAGGGCCAAGTGTACATCCTCGGCCGGGAGTCCCCACTGTCTCTCTACAA 1112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   366 rGiuGiuTyrAlaThrPheGlyGluAspLysValTyrLysGlnSerAspA 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  350 LysGlySerValThrAlaValGlnLysLysSerProAsnSerLeuTyrSe 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     333 laAspSerLeuSerLeuGluIleThrGlyGluValIleLeuLysLeuTyr 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                316 lTyrAspGlyArgTrpPheSerProIleArgLysSerLeuGlnAlaAlaA 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        963 GTATACCGGTTTACGGCCTAGCCCTGAGTGTGAATTTGTCCGCCACTGCA 1012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      300 GluSerPheArgTrpArgGluLysIleGlyLeuGluMetSerSerIleVa 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                913 GAAGTGCGCAAAATCAAACAAGGCCTGGGCTTGAAATTTGCTGAGCTGGT 962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Quality:
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2.741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Identity: 41.832
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Page 15

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103 TyrTyrAlaGluLysPheAsnAlaAspTyrValAlaHisGlySerThrGl 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               260 ACCTCCTGGGCACCTCTCTTGCCAGGCCCTGCATCGCCCGCAAACAACTG 309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     410 CCCAGATAAAGGTCATTGCTCCCTGGAGGATGCCTGAATTCTACAACCGG 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               460 TTCAAGGGCCGCAATGACCTGATGGAGTACGCAAAGCAACACGGGATTCC 509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |::: :::||| ::::::|||:::|||:::||||:::|||| 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   510 CATCCCGGTCACTCCCAAGAACCCGTGGAGGATGAGAACCTCATGC 559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         :::||| ||||:::||| ||||||:::||| :::::: |||
182 lyValSerIleGluCysGlyProLeuGluAspProTrpGlnGluProPro 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 560 ACATCAGCTACGAGGCTGGAATCCTGGAGAACCCCAAGAACCAAGCGCCT 609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                610 CCAGGTCTCTACACGAAGACCCAGGACCCAAGCCAAAGCCCCGCAACACCCC 659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        660 TGACATTCTCGAGATCGAGTTCAAAAAAGGGGTCCCTGTGAAAGGTGACCA 709
                                                                                                                                                                                                                                                                                                                                 710 ACGTCAAGGATGGCACCACCACCAGACCTCCTTGGAGCTCTTCATGTAC 759
                                                                                                                                                                                                                                                                                                                                                                                                                                        215 oGluTyrValThrValGlyPheGluLysGlyLysProValTyrLeu.... 230
                                                                                                                                                                                                                                                                                                                                                                                     231 ......AsnGlyGluArgTyrGluGluGlnTrpLysLeuIleAlaAsn 244
                                                                                                                                                                                                                                                                              810 GAACCGCTTCATTGGAATGAAGTCCCGAGGTATCTACGAGACCCCAGCAG 859
                                                                                                                                                                                                                                                       860 GCACCATCCTTTACCATGCTCATTTAGACATCGAGGCCTTCACCATGGAC 909
                                                                                                  1007 ACTECATCECCAAGTCCCAGGAGCGAGTGGAAAGGGAAAGTGCAGGTGTCC 1056
                                                                                                                                                                                                    910 CGG...GAAGTGCGCAAAATCAAACAAGGCCTGGGCTTGAAATTTGCTGA 956
                                                                                                                                                                                                                               278 lametValleuTyrGluAlaTyrArgAspLeuLeuSerLeuValLeuAsp 294
                                                 1057 GTCCTCAAGGGCCAGGTGTACATCCTCGGCCGGGAGGTCCCCACTGTCTCT 1106
                                                                                                                                                                             295 ArgPheThrPheHisTyrPheLeuThrHisIleProHisGluTyrAlaLy 311
                                                                                                                                                    957 GCTGGTGTATACCGGTTTACGGCCTAGCCCTGAGTGTGAATTTGTCCGCC 1006
1107 CTACAATGAGGAGCTGGTGAGCATGAACGTGCAGGGTGATTATGAGCCAA 1156
                                                                          311 sLeuValTyrGluGlyLeuTrpPheThrProLeuArgGluAlaLeuAspA 328
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Swissprot 39: ASSY_MOUSE + 2007.3.00 2246.54 4.

Swissprot 39: ASSY_BOVIN + 2069.00 2242.21 7.

Swissprot 39: ASSY_BOVIN + 2069.00 2242.21 7.

Swissprot 39: ASSY_SCHPO + 1083.00 1174.51 2.

Swissprot 39: ASSY_SCHPO + 1083.00 1174.51 2.

Swissprot 39: ASSY_ARATH + 911.50 986.80 5.

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Swissprot 39: ASSY_BUCAI + 777.00 843.39 6.

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Swissprot 39: ASSY_SYNY3 + 764.00 849.77 4.

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Swissprot 39: ASSY_METUA + 747.00 810.97 8.

Swissprot 39: ASSY_METUA + 747.00 810.97 8.

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Swissprot 39: ASSY_STRLA + 380.00 448.42 2.

Swissprot 39: ASSY_STRCA + 150.00 146.47 0.

Swissprot 39: ASSY_STRCA + 150.00 146.47 0.
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Swissprot_39:DRPL_RUMAN + 139.
Swissprot_39:DRPL_HUMAN + 139.
Swissprot_39:GLT4 WHEAT + 136.
Swissprot_39:GLT4 WHEAT + 136.
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Swissprot_39:GLT3 WHEAT + 134.
Swissprot_39:MY15_MOUSE + 134.
Swissprot_39:MY15_MOUSE + 134.
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Swissprot_39:ASSY_CORGL + 6
Swissprot_39:ASSY_PASMU + 4
Swissprot_39:ASSY_PASMU + 4
Swissprot_39:ASSY_ECOLI + 4
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Swissprot_39:ASSY_STRLA + 8
Swissprot_39:ASSY_STRLA + 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Command line parameters:
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Database sequences: 100059
Database length: 3664827
Search time (sec): 71.550000
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-DB=ScvissProt_39 -QFMT=fastan -SUFFIX=rsp -GAPOP=12.000
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-QGAPEXT=0.000 -YGAPEXT=0.000 -XGAPEXT=0.500
-FGAPOP=4.500 -QGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
-FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=10.000
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-TRANS=human40.cd1 -LIST=45 -DOCALIGN=200 -THR_SCORE=pct
-THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFWT=pfs
-NORM=ext -MINLEN=0 -MAXLEN=2000000000
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3.0e-63
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4.3e-38
3.9e-37
8.3e-35
2.0e-34
1.8e-31
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6.0e-18
6.0e-18
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5.2e-48
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                                                                                                                                                                                                                                            412 | p09034 rattus norregious (rat)
412 | p16460 mus musculus (mouse).

411 | p16460 mus musculus (mouse).

412 | p14568 bos taurus (bovine).

419 | 097069 drosophila melanogast
410 | 094354 schizosaccharomyces
410 | 094354 schizosaccharomyces cerevis
420 | p22768 saccharomyces cerevis
420 | p2718 saccharomyces cerevis
421 | 09523 arabidopsis thaliana
403 | p57158 buchnera aphidicola
403 | p57159 lactococcus lactis (s
400 | p77973 synechocystis sp. (st
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400 | p27979 lactococcus yanniel
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401 | 026072 methanocacrina barker
4039 | 1913256 methanocacrina barker
4040 | p7973 methanosacrina barker
405 | p9hkfl thermoplasma acidophi
406 | p13257 methanosacrina barker
407 | p3096 streptomyces clavulig
407 | p34315 haemophilus influenza
408 | p24767 escherichia coli. arg
408 | p24532 streptomyces lavendul
409 | p24532 streptomyces lavendul
400 | p24532 streptomyces (human)
401 | 006734 streptomyces (human)
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                                                            P10387 triticum aestivum (WI
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P10161 homo sapiens
                                                                                                   P04280 homo sapiens
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P08489 triticum aestivum (w
                Q9qzz4 mus musculus (mouse
59491 lactococcus lactis (su
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                                                                                                                                                                                                                                  52 homo sapiens (human).
epstein-barr virus (str
                                                                                                                                                                                           rattus norvegicus (ra
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                    SwissProt_39:GLT5_WHEAT +
SwissProt_39:SMF1_HUMAN +
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SwissProt_39:EXTN_TOBAC +
SwissProt_39:GLT5_WHEAT +
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"Sequence for
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                                                                                                                                                                                                                                                            "Mutations in argininosuccinate synthetase mRNA of Japanese patients, causing classical citrullinemia.";
Am. J. Hum. Genet. 55:1103-1112(1994).
                                                                                                                                                                                                                                                                                                                          VARIANTS THR-118; VAL-192; CYS-272; ARG-280; TRP-304 AND LEU-363. MEDLINE=95067972; PubMed=7977368; Kobayashi K., Shaheen N., Terazono H., Saheki T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kobayashi K., Jackson M.J., Tick D.B., O'Brien W.E., Beaudet A.L.; "Heterogeneity of mutations in argininosuccinate synthetase causing
                                                                                                                                                                    Shaheen N., Kobayashi K., Terazono H., Fukushige T., Horiuchi M.,
                                                                                                                                                                                                CHARACTERIZATION OF SOME VARIANTS. MEDLINE=96385010; PubMed=8792870;
                                                                                                                                                                                                                                                                                                                                                                                                                                         citrullinemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kobayashi K., Rosenbloom C., Beaudet A.L., O'Brien W.E.; "Additional mutations in argininosuccinate synthetase causing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=92048472; PubMed=1943692;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human citrullinemia."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-90293089;
                                                                                 Enzyme Protein 48:251-264(1995)
                                                                                                        synthetase proteins expressed in bacterial
                                                                                                                                                      Saheki T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VARIANTS LEU-18 AND CYS-86.
                                                                                                                               "Characterization of human wild-type and mutant argininosuccinate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biol. Chem. 265:11361-11367(1990).
                  PATHWAY: UREA CYCLE, PENULTIMATE STEP OF THE ARGININE BIOSYNTHETIC
                                                                CATALYTIC ACTIVITY: ATP + L-CITRULLINE + L-ASPARTATE =
                                           PYROPHOSPHATE + L-ARGININOSUCCINATE
                                                                                                                                                                                                                                                                                                                                                                                                                  Biol. Med. 8:95-100(1991).
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1 Q9y573 homo sapiens (huma
1 P13983 nicotiana tabacum
1 P10388 triticum aestivum
1 O14497 homo sapiens (hum
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21-JUI-1986 (Rel. 01, Created)
21-JUI-1986 (Rel. 01, Last Sequence update)
20-JUI-1986 (Rel. 01, Last sequence update)
20-JUI-1986 (Rel. 40, Last annotation update)
ARGININOSUCCINATE SYNTHASE (EC 6.3.4.5) (CITRULLINE--ASPARTATE
                                                                     TISSUE=Colon carcinoma;
MEDLLNE=97295306; PubMed=9150948;
Ji H., Reid G.E., Moritz R.L., Eddes J.S., Burgess A.W., Simpson R.J.;
"A two-dimensional gel database of human colon carcinoma proteins.";
Electrophoresis 18:605-613(1997).
                                                                                                                                                                                                                                                                                              "Molecular structures of human argininosuccinate synthetase pseudogenes. Evolutionary and mechanistic implications."; J. Biol. Chem. 259:3160-3166(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=84015388; PubMed=6194510;
BOCK H.-G.O., Su T.-S., O'Brien W.E., Beaudet A.L.;
VARIANTS S-14; H-157; N-180; S-324; W-304; W-363 AND R-390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            human argininosuccinate synthetase cDNA."; Res. 11:6505-6512(1983).
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alignment_block:
US-09-775-693-1 x ASSY_HUMAN
                                                                                          alignment_scores
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Ratio: 5.204
Percent Similarity: 100.000
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EMBL; L00084; AAA51783.1; -.
EMBL; L00079; AAA51783.1; JOINED.
EMBL; L000080; AAA51783.1; JOINED.
EMBL; L00081; AAA51783.1; JOINED.
EMBL; L00082; AAA51783.1; JOINED.
EMBL; L00083; AAA51783.1; JOINED.
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Pfam; PF00764; Arginosuc_synth; 1.
ProDom; PD003544; Arginosuc_synth; 1.
PROSITE; PS00564; ARGININOSUCCIN_SYN_1; 1.
PROSITE; PS00565; ARGININOSUCCIN_SYN_2; 1.
Arginine biosynthesis; Urea cycle; Ligase; ATP-binding;
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DISEASE: DEFECTS IN ASS ARE THE CAUSE OF CITRULLINEMIA, AN AUTOSOMAL RECESSIVE DISEASE CHARACTERIZED BY SEVERE VOMITING SPELLS AND MENTAL RETARDATION.

SIMILARITY: BELONGS TO THE ARGININOSUCCINATE SYNTHASE FAMILY.
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215700; -.
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R -> W (IN CITRULLINEMIA)
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S -> I. /TW
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G -> R (IN CITRULLINEMIA)
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G -> R (IN CITRULLINEMIA)
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G -> S (IN CITRULLINEMIA)
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hrProAlaGlyThrIleLeuTyrHisAlaHisLeuAspIleGluAlaPhe
                                                 PheMetTyrLeuAsnGluValAlaGlyLysHisGlyValGlyArgIleAs
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01-NOV-1988 (Rel. 09, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
ARGININOSUCCINATE SYNTHASE (EC 6.3.4.5) (CITRULLINE--ASPARTATE
EMBL; X12459; CAA30999.1; -.
EMBL; M36708; AAA40771.1; -.
PIR; S01440; AJRTRS.
InterPro; IPR001518; Arginosuc_synth. 1.
PfoDom; PD003544; Arginosuc_synth; 1.
ProDom; PD003544; Arginosuc_synth; 1.
PROSITE; PS00564; ARGININOSUCCIN_SYN_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
Mammalia, Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Ral
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                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration the Swiss Institute of Bioinformatics and the EMBL outstation between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its the European Bioinformatics Institute as its content is in no way the by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial used by an its statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                              MEDLINE-89016648; PubMed-3174461;
Surh L.C., Morris S.M., O'Brien W.E., Beaudet A.L.;
"Nucleotide sequence of the cDNA encoding the rat argininosuccinate
                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -i- SIMILARITY: BELONGS TO THE ARGININOSUCCINATE SYNTHASE FAMILY.
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SUBUNIT: HOMOTETRAMER
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Arginine biosynthesis; Urea cycle; Ligase; ATP-binding.
Arginine biosynthesis; Urea Cycle; Ligase; ATP-binding.
ATP (POTENTIAL),
NP_BIND 115 123 ATP (POTENTIAL),
SEQUENCE 412 AA; 46496 MW; CCA809006F5A3E93D CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34 yrLeualaasoiledlyGlnLysGluaspPheGluGlualaargLysLys 50
                                                                                                                                                                                                                                                                                                                                                          101 LysginvalGluileAlaglnArgGluGlyAlaLysTyrValSerHisGl 117
                                                                                                                                                                                                                                                                                                                                                                     301 AAACAAGTGGAAATCGCCCAGCGGGAGGGGGCCAAGTATGTGTCCCACGG 350
                                                                                                                                                                                                                                                                                                                                                                                                                               251 AGGACCGCTACCTCCTGGGCACCTCTCTTGCCAGGCCCTGCATCGCCCGC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      351 CGCCACAGGAAAGGGGAACGATCAGGTCCGGTTTGAGCTCAGCTACT 400
                                                                                                                                                                                                                                                                                                                                                                                                         117 yalaThrGlyLysGlyAsnAspGlnValArgPheGluLeuThrCysTyrS 134
                                                                                                                                                                                                                                      451 TACAACCGGTTCAAGGGCCGCAATGACCTGATGGAGTACGCAAAGCAACA 500
                                                                                                                                                                                                                                                                                      401 CACTGGCCCCCCAGATAAAGGTCATTGCTCCCTGGAGGATGCCTGAATTC 450
                                                                                                                                                                                                              151 TyrasnargPheLysGlyArgAsnaspLeuMetGluTyralaLysGlnHi 167
                                                                                                                                                                  501 CGGGATTCCCATCCCGGTCACTCCCAAGAACCCCGTGGAGCATGGATGAGA 550
                                                                                                                 551 ACCTCATGCACATCAGCTACGAGGCTGGAATCCTGGAGAACCCCCAAGAAC 600
                                                                   601 CAAGCGCCTCCAGGTCTCTACACGAAGACCCAGGACCCAGGCCAAAGCCCC 650
                      651 CAACACCCCTGACATTCTCGAGATCGAGTTCAAAAAAAGGGGTCCCTGTGA 700
701 AGGTGACCAACGTCAAGGATGGCACCACCCACCAGACCTCCTTGGAGCTC 750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ուսսունունունունունունունունունին
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                                                                                                                                                                                                                                Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   percent Identity: 96.845
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seq_documentation_block;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_name: SwissProt_39:ASSY_MOUSE
-!- SUBUNIT: HOMOTETRAMER.
-!- SIMILARITY: BELONGS TO THE ARGININOSUCCINATE SYNTHASE FAMILY.
                                            ·!- PATHWAY: UREA CYCLE, PENULTIMATE STEP OF THE ARGININE BIOSYNTHETIC
                                                              Gene 99:181-189(1991)
-!- CATALYTIC ACTIVITY: ATP + L-CITRULLINE + L-ASPARTATE = AMP +
PYROPHOSPHATE + L-ARGININOSUCCINATE.
                                                                                                                           MEDLINE=91216457; PDDMed=1708740; Surh L.C., Beaudet A.L., O'Brien W.E.; "Molecular characterization of the murine argininosuccinate synthetase locus.";
                                                                                                                                                                                                                                                                                                          P16460;
P16460;
O1-AUG-1990 (Rel. 15, Created)
O1-AUG-1990 (Rel. 15, Last sequence update)
15-UL-1999 (Rel. 38, Last annotation update)
ARGININOSUCCINATE SYNTHASE (EC 6.3.4.5) (CITRULLINE--ASPARTATE
                                                                                                                                                                                                                                 Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                          SEQUENCE FROM N.A. STRAIN-DBA/2J; TIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1201 GAATATCATCGTCTCCAGAGCAAGGTCACTGCCAAA 1236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1151 AGCCAACTGATGCCACCGGGTTCATCAACATCAATTCCCTCAGGCTGAAG 1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1101 GTCTCTCTACAATGAGGAGCTGGTGAGCATGAACGTGCAGGGTGATTATG 1150
                                                                                                                                                                                                                                                                                                                                                                                                                                        ASSY_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 401 GluTyrHisArgLeuGlnSerLysValThrAlaLys 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     384 luProlleAspAlaThrGlyPhelleAsnIleAsnSerLeuArgLeuLys 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1051 GTGTCCGTCCTCAAGGGCCAGGTGTACATCCTCGGCCGGGAGTCCCCACT 1100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     367 uSerLeuTyrAsnGluGluLeuValSerMetAsnValGlnGlyAspTyrG 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1001 TCCGCCACTGCATCGCCAAGTCCCAGGAGCGAGTGGAAGGGAAAGTGCAG 1050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  351 valSerValpheLysGlyGlnValTyrTleLeuGlyArgGluSerProLe 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  334 alArgHisCysTleAspLysSerGlnGluArgValGluGlyLysValGln 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               317 eAlaGluLeuValTyrThrGlyPheTrpHisSerProGluCysGluPhev 334
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                901 ACCATGOACCGGGAAGTGCGCAAAATCAAACAAGGCCTGGGCTTGAAATT 950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                301 ThrmetAspArgGluValArgLysIleLysGlnGlyLeuGlyLeuLysph 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             751 TTCATGTACCTGAACGAAGTCGCGGGCCAATGGCGTGGGCCGTATTGA 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            251 PheMetTyrLeuAsnGluValAlaGlyLysHisGlyValGlyArgIleAs 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
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alignment_block:
US-09-775-693-1 x ASSY_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to: ASSY_MOUSE from: 1 to: 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_scores:
451 TACAACCGGTTCAAGGGCCGCAATGACCTGATGGAGTACGCAAAGCAACA 500
                           134 erLeuAlaProGlnIleLysValIleAlaProTrpArgMetProGluPhe 150
                                             401 CACTGGGCCCCCAGATAAAGGTCATTGCTCCCTGGAGGATGCCTGAATTC 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity: 98.786
                                                                                                         351 CGCCACAGGAAAGGGGAACGATCAGGTCGGGTTTGAGCTCAGCTGCTACT 400
                                                                                        117 yAlaThrGlyLysGlyAsnAspGlnValArgPheGluLeuThrCysTyrs 134
                                                                                                                                                      101 ArgGlnValGluileAlaGlnArgGluGlyAlaLysTyrValSerHisGl
                                                                                                                                                                      301 AAACAAGTGGAAATCGCCCAGCGGGGGGGGGGGGGCCAAGTATGTGTCCCACGG 350
                                                                                                                                                                                                                                 251 AGGACGCTACCTCCTGGGCACCTCTCTTGCCAGGCCCTGCATCGCCGC 300
                                                                                                                                                                                                                                                                                                                                                           151 GCACTGAAGCTTGGGGCCAAAAAGGTGTTGATTGAGGATGTCACCAGGGA 200
                                                                                                                                                                                                                   84 luaspargTyrLeuLeuGlyThrSerLeuAlaArgProCysIleAlaArg 100
                                                                                                                                                                                                                                                                                                             67 uPheValGluGluPheIleTrpProAlaValGlnSerSerAlaLeuTyrG 84
                                                                                                                                                                                                                                                                                                                                                                                                                           101 ATCTGGCCAACATTGGCCAGAAGGAAGACTTCGAGGAAGCCAGGAAGAAG 150
                                                                                                                                                                                                                                                                                                                                             51 AlaLeuLysLeuGlyAlaLysLysValPheTleGluAspValSerLysGl 67
                                                                                                                                                                                                                                                                                                                                                                                                        34 yrLeuAlaAsnIleGlyGlnLysGluAspPheGluGluAlaArgLysLys 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17 rSerCysIleLeuValTrpLeuLysGluGlnGlyTyrAspValIleAlaT 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51 CTCGTGCATCCTCGTGTGGCTGAAGGAACAAGGCTATGACGTCATTGCCT 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M31690; AAA37266.1;

EMBL; M31692; AAB60707.1;

EMBL; M31694; AAB60708.1;

EMBL; M31693; AAB60708.1; JOINED

EMBL; M31695; AAB60708.1; JOINED

EMBL; M31702; AAB60706.1;

PIR; JU0463; AJMSRS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MGD; MGI:8090; ASS1.
InterPro; IPR001518; Arginosuc_synth.
Pfam; PF00764; Arginosuc_synth; 1.
ProDom; PD003544; Arginosuc_synth; 1.
PROSITE; PS00564; ARGININOSUCCIN_SYN_1; 1.
PROSITE; PS00565; ARGININOSUCCIN_SYN_2; 1.
Arginine biosynthesis; Urea cycle; Ligase; ATP-binding.
NP_BIND 115 123 ATP (POTENTIAL).
NP_BIND 115 123 ATP (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MetSerSerLysGlySerValValLeuAlaTyrSerGlyGlyLeuAspTh 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ATGTCCAGCAAAGGCTCCGTGGTTCTGGCCTACAGTGGCGGCCTGGACAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Quality: 2073.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Identity: 96.117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A8F3AFDDFBDAEF6A CRC64;
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seq_name: SwissProt_39:ASSY_BOVIN
          BBBBBBBB
                                                                                                                                                                                                                                        seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  551 ACCTCATGCACATCAGCTACGAGGCTGGAATCCTGGAGAACCCCCAAGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    601 CAAGCGCCTCCAGGTCTCTACACGAAGACCCAGGACCCAGCCAAAGCCCC 650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     651 CAACACCCCTGACATTCTCGAGATCGAGTTCAAAAAAGGGGTCCCTGTGA 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  701 AGGTGACCAACGTCAAGGATGGCACCACCCACCAGACCTCCTTGGAGCTC 750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1001 TCCGCCACTGCATCGCCAAGTCCCAGGAGCGAGTGGAAGGGAAAGTGCAG 1050
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                951 TGCTGAGCTGGTGTATACCGGTTTTACGGCCTAGCCCTGAGTGTGAATTTG 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              901 ACCATGGACCGGGAAGTGCGCAAAATCAAACAAGGCCTGGGCTTGAAATT 950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             284 hrProAlaGlyThrIleLeuTyrHisAlaHisLeuAspIleGluAlaPhe 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1151 AGCCAACTGATGCCACCGGGTTCATCAACATCAATTCCCTCAGGCTGAAG 1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1101 GTCTCTCTACAATGAGGAGCTGGTGAGCATGAACGTGCAGGGTGATTATG 1150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1201 GAATATCATCGTCTCCAGAGCAAGGTCACTGCCAAA 1236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       367 uSerLeuTyrAsnGluGluLeuValSerMetAsnValGlnGlyAspTyrG 384
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01-JAN-1990 (Rel. 13, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
argininosuccinate synthase (EC 6.3.4.5) (CITRULLINE--ASPARTATE LIGASE).
                                                                                                                                                                                                                                                                                                                                                                              401 GluTyrHisArgLeuGlnSerLysValThrAlaLys 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTCATGTACCTGAACGAAGTCGCGGGCAAGCATGGCGTGGGCCGTATTGA 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ysvalThrasnIleLysaspGlyThrThrargThrThrSerLeuGluLeu 250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   \verb|pileValGluAsnArgPheIleGlyMetLysSerArgGlyIleTyrGluT|
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       in in in international control of the control of th
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alignment_scores:
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US-09-775-693-1 x ASSY_BOVIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Align seg 1/1 to: ASSY_BOVIN from: 1 to: 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dennis J.A., Healy P.J., Beaudet A.L., O'Brien W.E.; "Molecular definition of bovine argininosuccinate synthetase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=90046714; PubMed=2813370;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9913;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute. There are no restrictions on its the European Bioinformatics Institute. There are no restrictions on its property institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SUBUNIT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRODUM; PD003544; Arginosuc_synth; 1.

PROSTTE; PS00564; ARGININOSUCCIN_SYN_2; 1.

PROSITE; PS00565; ARGININOSUCCIN_SYN_2; 1.

PROSITE; PS00565; ARGININOSUCCIN_SYN_2; 1.

Arginine biosynthesis; Urea cycle; Ligase; ATP-binding.

Arginine biosynthesis; Urea cycle; Ligase; ATP-binding.

NP_BIND 115 123 ATP (POTENTIAL).

NP_BIND 115 123 ATP (POTENTIAL).

SEQUENCE 412 AA; 46417 MW; 6F74C7F445EE0DB86 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; M26198; AAA30388.1; -. PIR; A33986; AJBORS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                            101 ATCTGGCCAACATTGGCCAGAAGAAGACTTCGAGGAAGCCAGGAAGAAG 150
                                                                                                                          151 GCACTGAAGCTTGGGGCCAAAAAGGTGTTCATTGAGGATGTCAGCAGGGA 200
                                                                                                                                                                                                                                                                                                                                                                                                                                           51 CTCGTGCATCCTCGTGTGGCTGAAGGAACAAGGCTATGACGTCATTGCCT 100
                                                                                                                                                                                                                                                                                                                 34 yrLeuAlaAsnIleGlyGlnLysGluAspPheGluGluAlaArgLysLys 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ATGTCCAGCAAAGGCTCCGTGGTTCTGGCCTACAGTGGCGGCCTGGACAC 50
251 AGGACCGCTACCTCCTGGGCACCTCTCTTGCCAGGCCCTGCATCGCCCGC 300
                                                                                                                                                                                       51 AlaLeuLysLeuGiyAlaLysLysValPheIleGluAspIleSerLysGl 67
                                                                DISEASE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HOMOTETRAMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Identity: 95.388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
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1151 AGCCAACTGATGCCACCGGGTTCATCAACATCAATTCCCTCAGGCTGAAG 1200
                                                                                      1101 GTCTCTCTACAATGAGGAGCTGGTGAGCATGAACGTGCAGGGTGATTATG 1150
                                                                                                                                                             1051 GTGTCCGTCCTCAAGGGCCAGGTGTACATCCTCGGCCGGGAGTCCCCACT 1100
                                                   1001 TCCGCCACTGCATCGCCAAGTCCCAGGAGCGAGTGGAAGGGAAAGTGCAG 1050
                                                                                                                         351 ValservaipheLysGlyGlnValTyrTieLeuGlyArgGluSerProLe 367
                                                                                                                                                                                              317 eAlaGluLeuValTyrThrGlyPheTrpHisSerProGluCysGluPheV 334
                                                                                                                                                                                                                                                                                                        951 TGCTGAGCTGGTGTATACCGGTTTTACGGCCTAGCCCTGAGTGTGAATTTG 1000
                                                                                                                                                                                                                                                                                                                                         301 ThrMetAspArgGluValArgLysIleLysGlnGlyLeuGlyLeuLysPh 317
                                                                                                                                                                                                                                                                                                                                                                             901 ACCATGGACCGGGAAGTGCGCAAAATCAAACAAGGCCTGGGCTTGAAATT 950
                                                                                                                                                                                                                                                                                                                                                                                                                284 hrProAlaGlyThrTleLeuTyTHisAlaHisLeuAspIleGluAlaPhe 300
                                                                                                                                                                                                                                                                                                                                                                                                                                   851 CCCCAGCAGGCACCATCCTTTACCATGCTCATTTAGACATCGAGGCCTTC 900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     267 prievalGluAsnArgPherleGlyMetLysSerArgGlyTleTyrGluT 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          801 CATCGTGGAGAACCGCTTCATTGGAATGAAGTCCCGAGGTATCTACGAGA 850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             251 PheLeuTyrLeuAsnGluValAlaGlyLysHisGlyValGlyArgIleAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              234 ysvalthrásnvalGlyAspGlyThrThrHisSerThrAlaLeuGluLeu 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   701 AGGTGACCAACGTCAAGGATGGCACCACCCACCAGACCTCCTTGGAGCTC 750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     217 oAsnSerProAspMetLeuGluIleGluPheLysLysGlyValProValL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        651 CAACACCCCTGACATTCTCGAGATCGAGTTCAAAAAAGGGGTCCCTGTGA 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         201 GlnAlaProProGlyLeuTyrThrLysThrGlnAspProAlaLysAlaPr 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               601 CAAGCGCCTCCAGGTCTCTACACGAAGACCCCAGGACCCAAAGCCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                184 snLeuMetHisIleSerTyrGluAlaGlyIleLeuGluAsnProLysAsn 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    551 ACCTCATGCACATCAGCTACGAGGCTGGAATCCTGGAGAACCCCCAAGAAC 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      501 CGGGATTCCCCATCCCGGTCACTCCCAAGAACCCCGTGGAGCATGGATGAGA 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         151 TyrasnargPheGlnGlyArgAsnAspLeuMetGluTyrAlaLysGlnHi 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               451 TACAACCGGTTCAAGGGCCGCAATGACCTGATGGAGTACGCAAAGCAACA 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  134 erLeuAlaProGlnIleLysValIleAlaProTrpArgMetProGluPhe 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 401 CACTGGCCCCCCAGATAAAGGTCATTGCTCCCTGGAGGATGCCTGAATTC 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       117 yalaThrGlyLysGlyAsnAspGlnIleArgPheGluLeuThrCysTyrS 134
351 CGCCACAGGAAAGGGGAACGATCAGGTCCGGTTTGAGCTCCAGCTGCTACT 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             301 AAACAAGTGGAAATCGCCCAGCGGGGGGGGGGGCCAAGTATGTGTCCCCACGG 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTCATGTACCTGAACGAAGTCGCGGGCAAGCATGGCGTGGGCCGTATTGA 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sGlyIleProValProValThrProLysAsnProTrpSerMetAspGluA 184
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Adams M.D. Cedniker S.E., Holt R.A., Evans C.A., Gocayne J.D., RA Adams M.D. Cedniker S.E., Elt R.A., Evans C.A., Gocayne J.D., RA Adams M.D. Cedniker S.E., Li P.W., Hoskins R.A., Galle R.F., RA Adams M.D., Cedniker S.E., Li P.W., Hoskins R.A., Galle R.F., RA Adams M.D., Cedniker S.E., Klohards S., Ashburner M., Henderson S.N., RA Gocrey R.A., Cherry M.D., Zhang Q., Chen L.X., RA Button G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., RA Button G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., RA Button G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., RA Button R.C., Royers Y.H.C., Blazel R.G., Champe M., Pfeiffer B.D., RA Double M.R., Doyle C., Baxendale J., Marker S.G., Helt G., Nelson C.R., Miklos G.L.G., RA Ballew R.M., Basu A., Baxendale J., Barker G.G., Petrick R. M. M. Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., RA Buttis K.C., Busam D.A., Butter H., Cadleu E., Center A., Chandra I., RA Borkova D., Datchan A.R., Bouck J., Brokstein P., Brottier P., Brottier R.A., Deng Z., Mays A.D., Dew I., Dietz S.M., RA Dodson K., Doup L.E., Downes M., Dugan Rocha S., Dunkov B.C., Dunn P., RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., RA Hiostin D., Houston K.A., Hoyland T.J., Wei M.-H., Diegwam C., RA Kinmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Guan P., Harris M., RA Hiostin D. M., Moharry C., Morris J., Moshrefi A., RA Meinto G.M., Mattei B., McIntosh T.C., McLeod M.P., Merberson D. M., Kalphy G., Merberson D. M., Weitser D., McHard J., Puri V., Reese M.G., Shapleton M., Skupski M.P., Smith T., RA RA Meinto G.M., Melson K.A., Murphy L., Muzny D., M., Nesson D.L., Ra Ra Hiostin G.S., Pan S., Pollard J., Puri V. Reese M.G., Shapleton M., Skupski M.P., Smith T., RA Mang S. M., Weitse B., Shan M., Wenter J., Shan M., Wang A.H., Wang S., Yao Q.A., Ra Mar
                         seq_documentation_block
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_name: SwissProt_39:ASSY_DROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Complete sequence of the Antennapedia complex of Drosophila.", Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             097069; 09VI41;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PROBABLE ARGININOSUCCINATE SYNTHASE (EC 6.3.4.5) (CITRULLINE--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Celniker S.E., Pfeiffer B., Knafels J., Martin C.H., Mayeda C.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1201 GAATATCATCGTCTCCAGAGCAAGGTCACTGCCAAA 1236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-BERKELEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ASPARTATE LIGASE).
BG:DS00004.14 OR CG13633.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         401 GluTyrHisArgLeuGlnAsnLysValThrAlaLys 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   384 luProValAspAlaThrGlyPheIleAsnIleAsnSerLeuArgLeuLys 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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alignment_scores:
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US-09-775-693-1 x ASSY_DROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Quality: 1164.00 Length: 405
Ratio: 3.571
Percent Similarity: 80.494 Percent Identity: 54.321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1 to: ASSY_DROME from: 1 to: 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration the Swiss Institute of Bioinformatics and the EMBL outstation between the Swiss Institute of Bioinformatics and the Exercitions on its the European Bioinformatics Institute. There are no restrictions on its the European Bioinformatics Institute as its content is in no way the by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseeisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -i- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
-i- SIMILARITY: BELONGS TO THE ARGININOSUCCINATE SYNTHASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -i- PATHWAY: UREA CYCLE, PENULTIMATE STEP OF THE ARGININE BIOSYNTHETIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AE001574; AAD19816.1; ALT_SEQ. EMBL; AE003674; AAF54103.1; ALT_SEQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Prodom; PD003544; Arginosuc_synth; 1.
PROSITE; PS00564; ARGININOSUCCIN_SYN_2; 1.
PROSITE: PS00565; ARGININOSUCCIN_SYN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arginine biosynthesis; Urea cycle; Ligase; Arp-binding.
NP_BIND 114 122 ATP (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pfam; pF00764; Arginosuc_synth;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FlyBase; FBgn0026565; BG:DS00004.14.
InterPro; IPR001518; Arginosuc_synth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE 419 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   110 ACATTGGCCAGAAGGAAGACTTCGAGGAAGCCAGGAAGAAGGCACTGAAG 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10 AAAGGCTCCGTGGTTCTGGCCTACAGTGGCGGCCTGGACACCTCGTGCAT 59
                                                                                                                                                                                                                                                                                                                                                                                               160 CTTGGGGCCAAAAAGGTGTTCATTGAGGATGTCAGCAGGGAGTTTGTGGA 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60 CCTCGTGTGGCTGAAGGAACAAGGCTATGACGTCATTGCCTATCTGGCCA 109
                                                                                                                                                                                                                                                                                                                                                                                                                                  210 GGAGTTCATCTGGCCGGCCATCCAGTCCAGCGCACTGTATGAGGACCGCT 259
                                                                                                                                                                                                                                                                 260 ACCTCCTGGGCACCTCTCTTGCCAGGCCCTGGATCGCCCGCAAACAAGTG 309
                                                                                                                                                                                                                                                                                                                                                               53 IleGlyAlaLysLysValIleValAlaAspValLysGlnSerPheValGl 69
                                                                                                                                                                                                310 GAAATCGCCCAGCGGGAGGGGGCCAAGTATGTGTCCCACGGCGCCACAGG 359
                                                                                                                               360 AAAGGGGAACGATCAGGTCCGGTTTGAGCTCAGCTGCTACTCACTGGCCC 409
                                                                                                                                                               103 GluvalAlaArgGluTyrGlyAlaLySTyrLeuAlaHisGlyAlaThrGl 119
                                                                                                                                                                                                                                                                                                69 uAspTyrIleTrpProAlaValGinMetGlyLeuValTyrGiuGluArgT 86
                                                410 CCCAGATAAAGGTCATTGCTCCCTGGAGGATGCCTGAATTCTACAACCGG 459
                                                                                                86 yrLeuLeuGlyThrSerLeuAlaArgProCysIleSerValAlaLeuMet 102
460 TTCAAGGGCCGCAATGACCTGATGGAGTACGCAAAGCAACACGGGATTCC 509
                                 roaspLeuLysIleIleAlaProTrpargaspValGluPheCysCysGln 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   46594 MW;
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510 CATCCCGGTCACTCCCAAGAACCCGTGGAGGATGGATGAGAACCTCATGC 559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            169 uValSerAlaLysProAlaThrProTrpSerThrAspAlaAsnIleLeuH 186
                                                                                                                             seq_name: SwissProt_39:ASSY_SCHPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                560 ACATCAGCTACGAGGCTGGAATCCTGGAGAACCCCAAGAACCAAGCGCCT 609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  610 CCAGGTCTCTACACGAAGACCCAAGGCCCA...GCCAAAGCCCCCAACAC 656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       203 GluAsnLeuTyrGluMetThrValAspProLeuThrArgAlaProArgAs 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            219 pProValHisLeuValIleGlnPheAspArgGlyLeuProSerSerValG 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         657 CCCTGACATTCTCGAGATCGAGTTCAAAAAAAGGGGTCCCCTGTGAAGGTGA 706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               707 CCAACGTCAAGGATGGCACCACCACCAGACGTCCTTGGAGCTCTTCATG 756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                236 luaspLeuProGlyGlyargValTyrThrLysProLeuGluMetLeuAsp 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     253 PheLeuAsnLysLeuGlyGlySerTyrGlyIleGlyArgIleAspIleVa 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  757 TACCTGAACGAAGTCGCGGGCCAAGCATGGCGTGGGCCCGTATTGACATCGT 806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        807 GGAGAACCGCTTCATTGGAATGAAGTCCCGAGGTATCTACGAGACCCCCAG 856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           857 CAGGCACCATCCTTTACCATGCTCATTTAGACATCGAGGCCTTCACCATG 906
                                                                                                                                                                                                                                                                                                                                                                                                                                        1007 ACTGCATCGCCAAGTCCCAGGAGCGAAGGGAAAGGGAAAGTGCAGGTGTCC 1056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                286 lyGlyThrIleLeuPheAlaAlaHisGlnAspLeuGluValPheAlaLeu 302
                                                                                                                                                                                                                                                                                                              1102 ....TCTCTCTACAATGAGGAGCTGGTGAGCATGAACGTGCAGGGTGATT 1147
                                                                                                                                                                                                                                                                                                                                                                               1057 GTCCTCAAGGGCCAGGTGTACATCCTCGGCCGGGAGTCCCCACTG..... 1101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       319 pTyrValTyrAsnGlyPheTrpPheSerProGluAlaIleTyrAlaArgL 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    957 GCTGGTGTATACCGGTTTACGGCCTAGCCCTGAGTGTGAATTTGTCCGCC 1006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 303 AspargGluValLeuArgThrLysGlnValLeuArgAspArgMetAlaAs 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 907 GACCGGGAAGTGCGCAAAATCAAACAAGGCCTGGGCTTGAAATTTGCTGA 956
                                                                                                                                                                                                                                                                                                                                                                                                           1148 ATGAGCCAACTGATGCCACCGGGTTCATCAACATCAATTCCCCTCAGGCTG 1197
                                                                                                                                                                                                                                                                                   353 LeualaProGlyTyrCysArgAlaIleAlaArgLysAlaAlaLysAspVa 369
                                                                                                                                                                                            1198 AAGGAATATCATCGT 1212
                                                                                                                                                                                                                      386 yrValProGinAspAlaGlyGlyPheIleAlaileAsnAlaValArgIle 402
                                                                                                                                                              403 ArgGluHisValArg 407
           30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
30-MAY-2000 (Rel. 39, Last annotation update)
ARGININOSUCCINATE SYNTHASE (EC 6.3.4.5) (CITRULLINE--ASPARTATE
LIGASE).
                                                                                          SCHPO
                                                                                               STANDARD;
                                                                                                     PRT;
                                                                                                         410 AA.
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SPBC428.05C.

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alignment_block:
US-09-775-693-1 x ASSY_SCHPO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to: ASSY_SCHPO from: 1 to: 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity: 81.013 Percent Identity: 54.430
322 CGGGAGGGGCCAAGTATGTGTCCCACGGCGCCCACAGGAAAGGGGAACGA 371
                                                                                                                                           272 CCTCTCTTGCCAGGCCCTGCATCGCCCGCAAACAAGTGGAAATCGCCCAG 321
                                                                                       92 hrSerLeuAlaArgProIleIleAlaArgArgGinIleGlnIleAlaGlu 108
                                                                                                                                                                                                                                                              222 GCCGGCCATCCAGTCCAGCGCACTGTATGAGGACCGCTACCTCCTGGGCA 271
                                                                                                                                                                                                   75 eProAlaAlaGinAlaAsnAlaIleTyrGluAsnValTyrLeuLeuGlyT 92
                                                                                                                                                                                                                                                                                                                                                                        172 AAGGTGTTCATTGAGGATGTCAGCAGGAGTTTGTGGAGGAGTTCATCTG 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        122 AGGAAGACTTCGAGGAAGCCAGGAAGAAGGCACTGAAGCTTGGGGCCAAA 171
                                                                                                                                                                                                                                                                                                                      59 LysValTyrValGluAspLeuArgGluGluPheIleAsnAspThrValIl 75
                                                                                                                                                                                                                                                                                                                                                                                                                                42 lugluAspTrpAspAlaAlaArgGluLysAlaLeuLysValGlyAlaLys 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25 uIleGluGluGlyTrpGluValIleCysTyrMetAlaAsnValGlyGlnG 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  72 GAAGGAACAAGGCTATGACGTCATTGCCTATCTGGCCAACATTGGCCAGA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22 GTTCTGGCCTACAGTGGCGGCCTGGACACCTCGTGCATCCTCGTGTGGCT 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AL034382; CAA22280.1; -.
InterPro; IPR001518; Arginosuc_synth.
Pfam; PF00764; Arginosuc_synth; 1.
Probom; PD003544; Arginosuc_synth; 1.
PROSITE; PS00564; ARGININOSUCCIN_SYN1; 1.
PROSITE; PS00565; ARGININOSUCCIN_SYN1; 1.
Arginine biosynthesis; Urea cycle; Ligase; ATP-binding.
APBIND 116 124 ATP (POTENTIAL)
PROSITE: PS00565; ARGININOSUCCIN_SYN2; 1.
Arginine biosynthesis; Urea cycle; Ligase; ATP-binding.
PROSITE: PS00565; ARGININOSUCCIN_SYN2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9 ValleuAlaTyrSerGlyGlyLeuAspThrSerCysTleLeuAlaTrpLe 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the EUropean Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way the content in the content in the content in the content is in the content in the cont
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -1- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
-1- SIMILARITY: BELONGS TO THE ARGININOSUCCINATE SYNTHASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- PATHWAY: UREA CYCLE, PENULTIMATE STEP OF THE ARGININE BIOSYNTHETIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungl; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Quality: 1083.00
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seq_name: SwissProt_39:ASSY_YEAST
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                                                                                                           1116 GGAGCTGGTGAGCATGAACGTGCAGGGTGATTATGAGCCAACTGATGCCA 1165
                      390 erGlyPheileGlnIleGluSerMetArgLeuArg 401
                                                                                                                                                           373 uLysLeuSerSerMetAspGluLeuGlyGlyPheAspProThrTrpThrS 390
                                                                                                                                        357 AsnValThrValLeuGlyArgLysSerAspThrAlaHisLeuTyrAspGl 373
                                                                                                                                                                                                                                    340 alserGlnGluValValAsnGlyValValLysLeuSerValTyrLysGly 356
                                                                                                                                                                                                                                                                   323 nGlyGlnPhePheSerProCysThrArgMetLeuLeuAlaAlaAsnAsnV 340
                                                                                                                                                                                                                                                                                                 969 CGGTTTACGGCCTAGCCCTGAGTGTGAATTTGTCCGCCACTGCATCGCCA 1018
                                                                                                                                                                                                                                                                                                                                307 AlaLeuArgAspGlnPheValThrPheAsnLeuAlaLysIleLeuTyrAs 323
                                                                                                                                                                                                                                                                                                                                                              922 AAAATCAAA...CAAGGCCTGGGCTTGAAATTTGCTGAGCTGGTGTATAC 968
                                                                                                                                                                                                                                                                                                                                                                                             290 rgThrAlaHisMetAspLeuGluGlyLeuThrNetGluArgGluValArg 306
                                                                                                                                                                                                                                                                                                                                                                                                                         872 ACCATGCTCATTTAGACATCGAGGCCTTCACCATGGACCGGGAAGTGCGC 921
                                                                                                                                                                                                                                                                                                                                                                                                                                                      772 GCGGGCAAGCATGGCGTGGGCCGTATTGACATCGTGGAGAACCGCTTCAT 821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    257 AlaArgArgAsnGlyValGlyArgIleAspIleValGluAsnArgPheSe 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 ly...ThrPheSerGlyValValSerIlePheTyrGlnLeuAsnAlaIle 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              722 GCACCACCCACCAGACCTCCTTGGAGCTCTTCATGTACCTGAACGAAGTC 771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            225 rīleHisPheGluLysGlyAlaProThrLysLeu...GluCysLysAspG 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         672 GATCGAGTTCAAAAAAGGGGTCCCTGTGAAGGTGACCAACGTCAAGGATG 721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       209 LysLeuThrValAspProLysAspAlaProAspGluValGluGluLeuSe 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      622 ACGAAGACCCCAGGACCCAGGCCAAAGCCCCCAACACCCCTGACATTCTCGA 671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     192 luAlaGlyIleLeuGluAspProSerMetThrProProLysAspMetTrp 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       572 AGGCTGGAATCCTGGAGAACCCCAAGAACCAAGCGCCTCCAGGTCTCTAC 621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  522 TCCCAAGAACCCGTGGAGCATGGAGGATGAGAACCTCATGCACATCAGCTACG 571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                175 rThrLysLysProTrpSerMetAspGluAsnIleValHisCysSerTyrG 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             159 LysaspLeuLeuGluTyralaalaalaLysGlyIleProValThrGlnTh 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          472 AATGACCTGATGGAGTACGCAAAGCAACACGGGATTCCCCATCCCGGTCAC 521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          142 alileAlaProTrpArgLeuProValPhePheGluArgPheAlaGlyArg 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         422 TCATTGCTCCCTGGAGGATGCCTGAATTCTACAACCGGTTCAAGGGCCCGC 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    125 pGinValArgPheGluLeuAlaTyrTyrAlaLeuLysProAspValGlnV 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    372 TCAGGTCCGGTTTGAGCTCAGCTGCTACTCACTGGCCCCCAGATAAAGG 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               109 LysGluAsnCysIleAlaValSerHisGlyCysThrGlyLysGlyAsnAs 125
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seq_documentation_block:

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ASSY_YEAST STANDARD; PRT; 420 AA.
P22768;
P22768;
P3.4 (1991 (Rel. 19, Created)
P3.5 (Rel. 34, Last sequence update)
P3.5 (Rel. 34, Last annotation update)
P3.5 (CITRULLINE--ASPARTATE
PARGININOSUCCINATE SYNTHASE (EC 6.3.4.5) (CITRULLINE--ASPARTATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Saccharomycetales; Saccharomycetaceae; Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LIGASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nakamura Y., Baumberg S., Glansdorft N.;
"Sequences of the genes encoding argininosuccinate synthetase in
Escherichia coli and Saccharomyces cerevisiae: comparison with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  van Vliet F., Crabeel M., Boyen A., Tricot C., Stalon V., Falmagne P., Nakamura Y., Baumberg S., Glansdorff N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE=91071613; PubMed=2123815;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          methanogenic archaebacteria and mammals.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=96381248; PubMed=8789261;
Mannhaupt G., Vetter I., Schwarzlose C., Mitzel S., Feldmann H.;
Mannhaupt G. 26 kb region on the left arm of yeast chromosome XV.";
"Analysis of a 26 kb region on the left arm of yeast chromosome XV.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gene 95:99-104(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Crabeel M., Seneca S., Devos K., Glansdorff N.;
"Arginine repression of the Saccharomyces cerevisiae ARG1 gene.
Comparison of the ARG1 and ARG3 control regions.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 1-57 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yeast 12:67-76(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way use by non-profit institutions as long the swing of the swing as its content is in no way use by and this statement is not removed. Usage by and for commercial modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- PATHWAY: UREA CYCLE, PENULTIMATE STEP OF THE ARGININE BIOSYNTHETIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                          EMBL; M35237; AAA34437.1; ...
EMBL; X91067; CAA62528.1; ...
EMBL; Z74800; CAA99067.1; ...
EMBL; X07070; CAA39106.1; ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                     ProDom; PD003544; Arginosuc_synth; 1.
PROSTE; PS00564; ARGININOSUCCIN_SYN_1; 1.
                                                                                                                                                                                                                                                                                            Pfam; PF00764; Arginosuc_synth;
                                                                                                                                                                NP_BIND
                                                                                                                                                                                    Arginine biosynthesis; Urea
                                                                                                                                                                                                                    PROSITE;
                                                                                                                                                                                                                                                                                                                           InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OR YOL058W OR 01228.
                                                         CONFLICT
                                                                                CONFLICT
     SEQUENCE
                                     CONFLICT
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R. GENETION: IN YEAST, AS CAN HAVE A CATABOLIC FUNCTION SINCE IT FUNCTION: IN YEAST, AS CAN HAVE A CATABOLIC FUNCTION SINCE AND THE ARGINASE PARHMAY.

REACTIONS INVOLVED IN THE ARGINASE PARHMAY.

REACTIONS INVOLVED IN THE ARGINASE PARHMAY.

REACTIONS INVOLVED IN THE ARGINATE ARGINATE AMP + L-CITRULLINE + L-ASPARTATE = AMP + CATALYTIC ACTIVITY: AFF + L-CITRULLINE + L-ASPARTATE = AMP + CATALYTIC ACTIVITY: AFF + L-CITRULLINE + L-ASPARTATE = AMP + CATALYTIC ACTIVITY: AFF + L-CITRULLINE + L-ASPARTATE = AMP + CATALYTIC ACTIVITY: AFF + L-CITRULLINE + L-ASPARTATE = AMP + CATALYTIC ACTIVITY: AFF + L-CITRULLINE + L-ASPARTATE = AMP + CATALYTIC ACTIVITY: AFF + L-CITRULLINE + L-ASPARTATE = AMP + CATALYTIC ACTIVITY: AFF + L-CITRULLINE + L-ASPARTATE = AMP + CATALYTIC ACTIVITY: AFF + L-CITRULLINE + L-ASPARTATE = AMP + CATALYTIC ACTIVITY: AFF + L-CITRULLINE + L-ASPARTATE = AMP + CATALYTIC ACTIVITY: AFF + L-CITRULLINE + L-ASPARTATE + AMP + CATALYTIC ACTIVITY: AFF + L-CITRULLINE + L-ASPARTATE + AMP + CATALYTIC ACTIVITY: AFF + L-CITRULLINE + L-ASPARTATE + AMP + CATALYTIC ACTIVITY: ATF + L-CITRULLINE + L-ASPARTATE + AMP + CATALYTIC ACTIVITY: ATF + L-CITRULLINE + L-ASPARTATE + AMP + CATALYTIC ACTIVITY: ATF + L-CITRULLINE + L-ASPARTATE + AMP + CATALYTY + L-CITRULLINE + L-ASPARTATE + AMP + CATALYTY + AMP + L-CITRULLINE + L-ASPARTATE + AMP + CATALYTY + L-CITRULLINE + L-ASPARTATE + AMP + L-CITRULLINE + L-ASPARTATE + L-CITRULLINE + L-ASPARTATE + L-CITRULLINE +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: BELONGS TO THE ARGININOSUCCINATE SYNTHASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PYROPHOSPHATE + L-ARGININOSUCCINATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PATHWAY.
                                                                                                                                                                                                                                                                                                                                               S0005419;
                                                                                                                                                                                                                                                                                                                                                                               JQ0779; AJBYRS.
                                                                                                                                                                                                pS00565; ARGININOSUCCIN_SYN_2; 1.
blosynthesis; Urea cycle; Ligase; ATP-binding.
                                                                                                                                                                                                                                                                                                                     15419; ARG1.
1PR001518; Arginosuc_synth.
                 420 AA;
                    46939 MW;
                                           GY -> AT (IN REF. 1 AND 3).

EX -> VL (IN REF. 1 AND 3).

EX -> VL (IN REF. 1).

VDCR -> GGLS (IN REF. 1).

P -> F (IN REF. 1).

F -> L (IN REF. 1).
                                                                                                                                                                            ATP (POTENTIAL)
                    7E53C9DD58443860 CRC64;
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alignment_scores:
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US-09-775-693-1 x ASSY_YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ratio: 3.351 percent similarity: 77.053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Align seg 1/1 to: ASSY_YEAST from: 1 to: 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  107 CCAACATTGGCCAGAAGGAAGACTTCGAGGAAGCCAGGAAGAAGGCACTG 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              157 AAGCTTGCGGCCAAAAAGGTGTTCATTGAGGATGTCAGCAGGGAGTTTGT 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             207 GGAGGAGTTCATCTGGCCGGCCATCCAGTCCAGCGCACTGTATGAGGACC 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18 lIleLeuAlaTrpLeuLeuAspGinGlyTyrGluValValAlaPheMetA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57 CATCCTCGTGTGGCTGAAGGAACAAGGCTATGACGTCATTGCCTATCTGG 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  307 GTGGAAATCGCCCAGGGGAGGGGGGGCCAAGTATGTGTCCCACGGCGCCCAC 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           257 GCTACCTCCTGGGCACCTCTCTTGCCAGGCCCTGCATCGCCCGCAAACAA 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35 laAsnValGlyGlnGluGluAspPheAspAlaAlaLysGluLysAlaLeu 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 AGCAAAGGCTCCGTGGTTCTGGCCTACAGTGGCGGCCTGGACACCTCGTG 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         102 IleAspValAiaLysGlnGluGlyCysPheAlaValSerHisGlyCysTh 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            52 LysileGlyAlaCysLysPheValCysValAspCysArgGluAspPheVa 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        118 rGlyLysGlyAsnAspGinIleArgPheGluLeuSerPheTyrAlaLeuL 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68 ILYSASpIleLeuPheproAlaValGinValAsnAlaValTyrGiuAspV 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             135 ysproAspValLysCysileThrProTrpArgMetProGlubhePheGlu 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       407 CCCCCCAGATAAAGGTCATTGCTCCCTGGAGGATGCCTGAATTCTACAAC 456
                                                                                                                                                                                                                                                                                                                                    507 TCCCATCCCGGTCACTCCCAAGAACCCGTGGAGCATGGATGAGAACCTCA 556
                                                                                                                                                                                                                                    557 TGCACATCAGCTACGAGGCTGGAATCCTGGAGAACCCCAAGAACCAAGCG 606
                                                                                                                                                                                                                                                                                                     168 eProValalaGlnThrLysAlaLysProTrpSerThrAspGluAsnGlnA 185
                                                                                                                                                                                                     607 CCTCCAGGTCTCTACACGAAGACCCAGGACCCAAGCCCAAAGCCCCAACAC 656
                                                                                                                                  657 CCCTGACATTCTCGAGATCGAGTTCAAAAAAGGGGTCCCTGTGAAGGTGA 706
                                                                                                 218 nProGlnAspLeuThrileAspPheGluArgGlyLeuProValLysLeuT 235
745 GAGCTCTTCATGTACCTGAACGAAGTCGCGGGCAAGCATGGCGTGGGCCG
                               235 hrTyrThrAspAsaLysThrSerLysGluValSerValThrLysProLeu
                                                                  707 CCAACGTCAAGGATGGCACCACCACCAGACCTCC......TTG 744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGGAAAGGGGAACGATCAGGTCCGGTTTGAGCTCAGCTGCTACTCACTGG 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quality: 1069.00
                                                                                                                                                                                                                                                                                                                                                                                                       CGGTTCAAGGGCCGCAATGACCTGATGGAGTACGCAAAGCAACACGGGAT 506
                                                                                                                                                                    ProLysAspMetTrpLysLeuIleValAspProMetAspAlaProAspGl 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  percent Identity: 50.483
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seq_documentation_block:
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Kreis M., Delseny M., Puidomenech P., Watson M., Schmidtheini T., Reichert B., Porteteile D., Perez-Alonso M., Boutry M., Bancroft I., Vos P., Hoheisel J., Zimmermann W., Wedler H., Ridley P., Langham S.-A., McCullagh B., Bilham L., Robben J., Vandenbussche F., Van der Schueren J., Grymonprez B., Chuang Y.-J., Vandenbussche F., Braeken M., Weitjens I., Voet M., Bastiaens I., Aert R., Defoor E., Weitzenegger T., Bothe G., Ramsperger U., Hilbert H., Braun M., Holzer E., Brandt A., Peters S., van Staveren M., Dirkse W., Mooljman p., Klein Lankhorst R., Rose M., Hauf J., Koetter P., Berneiser S., Hempel S., Feldpausch M., Lamberth S., Van den Daele H., De Keyser A., Buysshaert C., Gielen J., Villarroel R., De Clercq R.,
                                                                                                                                                                                                                                                                                              STRAIN-CV. COLUMBIA;

MEDLING-20083488; PubMed=10617198;

Mayer K.F.X., Schueller C., Wambutt R., Murphy G., Volckaert G.,

Pohl T., Duesterhoeft A., Stiekema W., Entian K.-D., Terryn N.,

Pohl T., Duesterhoeft A., Grivell, Rieger M.,

Harris B., Ansorge W., Brandt P., Grivell, Rieger M.,

Weichselgartner M., de Simone V., Obermaler B., Mache R., Mueller M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation updat
ARGININOSUCCINATE SYNTHASE, CHLOROPLAST PRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CITRULLINE--ASPARTATE LIGASE).
AT4G24830 OR F617.40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1189 CTCAGGCTGAAGGAATATCATCGTCTCCAGAGCAAGGTCACT 1230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1139 AGGGTGATTATGAGCCAACTGATGCCACCGGGTTCATCAACATCAATTCC 1188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9SZX3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         402 IleArgIleLysLysTyrGly.....GluSerLysLysThr 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1092 GTCCCCACTG...TCTCTCTACAATGAGGAGCTGGGTGAGCATGAACGTGC 1138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            385 euThrGlyPheLeuProThrAspThrThrGlyPheIleAlaIleGlnAla 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1042 AAAGTGCAGGTGTCCGTCCTCAAGGGCCAGGTGTACATCCTCGGCCGGGA 1091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  368 rThrLysThrGluLysLeuTyrAspProThrGluSerSerMetAspGluL 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            352 ThrvalArgValArgLeuTyrLysGlyAsnValIleIleLeuGlyArgSe 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  335 ysGluTyrIleArgSerMetIleGlnProSerGlnAsnSerValAsnGly 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    992 GTGAATTTGTCCGCCACTGCATCGCCAAGTCCCCAGGAGCGAGTGGAAGGG 1041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           318 rProAsnTyrSerArgLeuIleTyrAsnGlyPheLeuLeuHisProGluC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             942 CTTGAAATTTGCTGAGCTGGTGTATACCGGTTTACGGCCTAGCCCTGAGT 991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               302 GlyLeuThrLeuAspLysGluValArgGlnLeuArgAspSerPheValTh 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                895 GCCTTCACCATGGACCGGGAAGTGCGCAAAATCAAACAAGGC...CTGGG 941
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    252 ASPValPheLeuAlaAlaSerAsnLeuAlaArgAlaAsnGlyValGlyAr 268
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               annotation update)
CHLOROPLAST PRECURSOR (EC 6.3.4.5)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    523 AA.
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alignment_block:
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US-09-775-693-1 x ASSY_ARATH
                                                                    Percent Similarity:
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RA Schnabl S. Hiller R., Schmidt W., Lecharny A., Aubourg S.,
RA Chefdor F., Cooke R., Berger C., Monfort A., Casacuberta E.,
RA Gibbons T., Weber N., Vandenbol M., Bargues M., Terol J., Torres A.,
RA Heijnen L., Schwarz S., Scholler P., Heber S., Francs P., Bielke C.,
RA Heijnen L., Schwarz S., Scholler P., Heber S., Francs P., Bielke C.,
RA Frishman D., Haase D., Lemcke K., Mewes H.-W., Stocker S.,
RA Parnell L., Dedhia N., Gnoj L., Schutz K., Huang E., Spiegel L.,
RA Zaccarla P., Bevan M., Wilson R.K., de la Bastide M., Habermann K.,
RA Schkon M., Murray J., Sheet P., Cordes M., Abu-Threideh J.,
RA Schking T., Kalicki J., Graves T., Harmon G., Edwards J.,
RA Minx P., Bentley L., Cloud J., Abbett A., Scott K., Johnson D.,
RA Kramer J., Fulton B., Miller N., Greco T., Kemp K.,
RA Kramer J., Fulton L., Mardis E., Dante M., Pepin K., Hillier L.,
RA Antonolu B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C.,
RA Antonolu B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C.,
RA Ma P., Zhong J., Preston R., Vil D., Shekher M., Matero A., Shah R.,
RA Granat S., Shohdy N., Hasegawa A., Hameed A., Lodhi M., Johnson A.,
RT "Sequence and analysis of chromosome 4 of the plant Arabidopsis
                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                 EMBL; AL049657; CAB41123.1; ALT_SEQ.
EMBL; AL161562; CAB79393.1; ALT_SEQ.
InterPro; IPR001518; Arginosuc_synth.
Pfam; PF00764; Arginosuc_synth; 2.
                                                                                                                                                                                                                              CHAIN
                                                                                                                                                                                                                                                     Arginine biosynthesis; Ligase; ATP-binding; Transit peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                TRANSIT
                                                                                                                                                                                                                                                                                                            PROSITE;
                                                                                                                                                                                                                                                                                                                            PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: CHLOROPLAST (POTENTIAL).
-!- SIMILARITY: BELONGS TO THE ARGININOSUCCINATE SYNTHASE FAMILY.
-!- CAUTION: REF. 1 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO WRONG EXON PREDICTIONS FROM THE GENOMIC SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished observations (JUN-2001).

-I- CATALYTIC ACTIVITY: ATP + L-CITRULLINE + L-ASPARTATE = AMP + PROPHOSPHATE + L-ARGININOSUCCINATE.

-I- PATHWAY: PENULTIMATE STEP IN ARGININE BIOSYNTHESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CONCEPTUAL TRANSLATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 402:769-777(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Van Montagu M., Rogers J., Cronin A., Quail M., Bray-Allen S., Clark L., Doggett J., Hall S., Kay M., Lennard N., McLay K., Mayes R., Pettett A., Rajandream M.-A., Lyne M., Benes V., Rechmann S., Borkova D., Bloecker H., Scharfe M., Girmm M., Loehnert T.-H., Dose S., de Haan M., Maarse A., Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Fartmann B., Granderath K., Dauner D., Herzl A., Massenet O., Quigley F., Clabauld G., Muendlein A., Felber R., Schnahl S., Hillar B., Chmidt G., Muendlein A., Felber R., Schnahl S., Hillar B., Chmidt G., Muendlein A., Felber R., Schnahl S., Hillar B., Chmidt G., Muendlein A., Felber R.,
                                                                                                              Quality:
                                                                                                                                                                                                                                                                                     PD003544; Arginosuc_synth; 1;
PS00564; ARGININOSUCCIN_SYN_1; 1;
PS00565; ARGININOSUCCIN_SYN_2; 1.
                                                                                           Ratio:
                                                                                                                                                                                              523 AA;
                                                                  911.50
3.018
76.263
                                                                                                                                                                                       523 AI
57249 MW;
                                                  Percent Identity: 45.707
                                                                                                                                                                                              CHLOROPLAST (POTENTIAL).
ARGININOSUCCINATE SYNTHASE.
                                                                                                                                                                           97B82A5A718969C8 CRC64;
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Align seg 1/1 to: ASSY_ARATH from: 1 to: 523
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         144 pLeuLysGiuAsnTyrGiyCysGluValValCysPheThrAlaAspValG 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          116 GCCAGAAG...GAAGACTTCGAGGAAGCCAGGAAGAAGGCACTGAAGCTT 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19 GTGGTTCTGGCCTACAGTGGCGGCCTGGACACCTCGTGCATCCTCGTGTG 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 163 GGGGCCAAAAAGGTGTTCATTGAGGATGTCAGCAGGAGTTTGTGGAGGA 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            161 iyGinGlyTleLySGluLeuGluGlyLeuGluGlnLySAlaLySAlaSer 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       69 GCTGAAGGAACAA...GGCTATGACGTCATTGCCTATCTGGCCAACATTG 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 178 GlyAlaSerGlnLeuValValLysAspLeuThrGluGluPheValLysAs 194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    213 GTTCATCTGGCCGGCCATCCAGTCCAGCGCACTGTATGAGGACCGCTACC 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       263 TCCTGGGCACCTCTTGCCAGGCCCTGCATCGCCCGCAAACAAGTGGAA 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          313 ATCGCCCAGCGGGAGGGGGCCAAGTATGTGTCCCACGGCGCCACAGGAAA 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        211 euLeuGlyThrSerMetAlaArgProValIleAlaLysAlaMetValAsp 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               363 GGGGAACGATCAGGTCCGGTTTGAGCTCAGCTGCTACTCACTGGCCCCCC 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             228 ValnianlaGluValGlyhlanspalaValalaHisGlyCysThrGlyLy 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  413 AGATAAAGGTCATTGCTCCCTGGAGGATGCCTGAATTCTACAACCGGTTC 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     463 AAGGGCCGCAATGACCTGATGGAGTACGCAAAGCAACACGGGATTCCCAT 512
                                                                                                                                                                                                                                                                                                                                                                                                                                         513 CCCGGTCACTCCCAAGAACCCGTGGAGGATGGATGAGAACCTCATGCACA 562
                                                                                                                                                                                                                                                                                                                                                                                                           290 lproValThrLysLysSerIleTyrSerArgAspArgAsnLeuTrpHist 307
                                                                                                                                                                                                                                                                                                                                                                            563 TCAGCTACGAGGCTGGAATCCTGGAGAACCCAAGAACCAAGCGCCTCCA 612
                                                                                                                                                                                                                                                                                                               613 GGTCTCTACACGAAGACCCAGGACCCAAGCCAAAGCCCCCAACACCCCCTGA 662
                                                                                                                                                                                                                                                   663 CATTCTCGAGATCGAGTTCAAAAAAAGGGGTCCCTGTGAAGGTGACCCAACG 712
                                                                                                                                                                                                                                                                                  324 ASPMetTyrMetMetSerValAspProGluAspAlaProAspGlnProGl 340
                                                                                                                                                                                                                       340 uTyrileGluileGlyIleGluSerGlyLeuProValAlaLeuAsnGly. 356
                                                                                                                                                                                         713 TCAAGGATGGCACCACCAGACCTCCTTGGAGCTCTTCATGTACCTG 762
                                                                                            369 AsnThrIleGlyGlyLysHisGlyIleGlyArgIleAspMetValGluAs 385
                                                                                                               763 AACGAAGTCGCGGGCAAGCATGGCGTGGGCCGTATTGACATCGTGGAGAA 812
                             813 CCGCTTCATTGGAATGAAGTCCCGAGGTATCTACGAGACCCCAGCAGGCA 862
   863 CCATCCTTTACCATGCTCATTTAGACATCGAGGCCTTCACCATGGACCGG 912
                                                                                                                                                                                                                                                                                                                                                euserHisGluGlyAspLeuLeuGluAspProAlaAsnGluProLysLys 323
                                                                                                                                                            ......LysAlaLeuSerProAlaThrLeuLeuAlaGluLeu 368
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seq_name: SwissProt_39:ASSY_BACSU
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   402 hrlleLeuPheAlaAlaValGlnGluLeuGluSerLeuThrLeuAspArg 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        963 GTATACCGGTTTACGGCCTAGCCCTGAGTGTGAATTTGTCCGCCACTGCA 1012
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1163 CCACCGGGTTCATCAACATCAATTCCCTCAGGCTGAAG 1200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        485 gGlnAspIleSerSerPheGluGlySerGluIleTyrAsnGlnAlaAspA 502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                502 laAlaGlyPheileArgLeuTyrGlyLeuProMetLys 514
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034347;
15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
20-AUG-2001 (Rel. 40, Last annotation update)
ARGININOSUCCINATE SYNTHASE (EC 6.3.4.5) (CITRULLINE--ASPARTATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lapidus A., Galleron N., Sorokin A., Ehrlich S.D.;

"Sequencing and functional annotation of the Bacillus subtilis genes
"Sequencing and functional annotation of the Bacillus subtilis genes
"Sequencing and functional region.";
in the 200 kb rnB-dnaB region.";
in t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bactleria; Firmicutes; Bacillus/Clostridium group; Bactlus/staphylococcus group; Bacillus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=1423
                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation its between the Swiss Institute of Broinformatics are no restrictions on its the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SIMILARITY: BELONGS TO THE ARGININOSUCCINATE SYNTHASE FAMILY.
PFam; PF00764; Arginosuc_synth; 1.
ProDom; PD003544; Arginosuc_synth; 1.
PRODOM; PD003544; ARGININOSUCCIN_SYN_2; 1.
PROSITE; PS00564; ARGININOSUCCIN_SYN_2; 1.
PROSITE; PS00565; ARGININOSUCCIN_SYN_2; 1.
Arginine biosynthesis; Ligase; ATP-binding; Complete proteome. Arginine biosynthesis; Ligase; ATP-binding; Complete Proteome. Arginine biosynthesis; Ligase; ATP-binding; CRC64; AGUUENCE 403 AA; 44817 MW; BEF522A77386111F CRC64;
                                                                                                                                                                                                                                                                                                                                                                               entitles requires a license agreement (% or send an email to license@isb-sib.ch).
                                                                                                                                                                                             SubtiList; BG12570; argG.
InterPro; IPR001518; Arginosuc_synth.
                                                                                                                                                                                                                                                          EMBL; Z99118; CAB14905.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                               license agreement (See http://www.isb-sib.ch/announce/
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751 TTCATGTACCTGAACGAAGTCGCGGGCAAGCATGGCGTGGGCCGTATTGA 800
                            229 erile.....AspGlyValSerTyrSerLeuSer...GluLeu 240
                                                           701 AGGTGACCAACGTCAAGGATGGCACCACCACCAGACCTCCTTGGAGCTC 750
                                                                                              212 oAspThrProGluValIleGluILeAlaPheGluGlnGlyValProValS 229
                                                                                                                          651 CAACACCCCTGACATTCTCGAGATCGAGTTCAAAAAAGGGGGTCCCTGTGA 700
                                                                                                                                                        196 AlaProProGluGlyAlaTyrAspLeuThrAlaProLeuGluLysThrPr 212
                                                                                                                                                                                      601 CAAGCGCCTCCAGGTCTCTACACGAAGACCCAGGACCCAGCCAAAGCCCC 650
                                                                                                                                                                                                                     179 snLeuTrpGlyArgAlaAsnGluCysGlyIleLeuGluAspProTrpAla 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_block:
US-09-775-693-1 x ASSY_BACSU
                                                                                                                                                                                                                                                   551 ACCTCATGCACATCAGCTACGAGGCTGGAATCCTGGAGAACCCCAAGAAC 600
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                                                                                                                                                                                                                                                                                                               501 CGGGATTCCCCATCCCGGTCACTCCCCAAGAACCCGTGGAGCATGGATGAGA 550
                                                                                                                                                                                                                                                                                                                                            151 ......SerArgGluGluGluIleGluTyrAlaAlaSerAr 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Align seg 1/1 to: ASSY_BACSU from: 1 to: 403
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                                                                                                                                                                                                                                                                                                                                                                            451 TACAACCGGTTCAAGGGCCGCAATGACCTGATGGAGTACGCAAAGCAACA 500
                                                                                                                                                                                                                                                                                                                                                                                                           134 erLeuAsnProAspLeuGluValīleAlaProValArgGluTrpGlnTrp 150
                                                                                                                                                                                                                                                                                                                                                                                                                                         401 CACTGGCCCCCCAGATAAAGGTCATTGCTCCCTGGAGGATGCCTGAATTC 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Quality: 818.00
Ratio: 2.773
Percent Similarity: 73.750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         117 yCysThrGlyLysGlyAsnAspGlnValArgPheGluValSerIleLysS 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          351 CGCCACAGGAAAGGGGAACGATCAGGTCCGGTTTGAGCTCAGCTGCTACT 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   101 LysLeuValGlurieAlaGluLysGluAspAiaGlnAlaTleAlaHisGi 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        301 AAACAAGTGGAAATCGCCCAGCGGGAGGGGGGCCAAGTATGTGTCCCACGG 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               251 AGGACCGCTACCTCCTGGGCACCTCTCTTGCCAGGCCCTGCATCGCCCGC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84 luGlyLysTyrProLeuValSerAlaLeuSerArgProLeuIleAlaLys 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67 uPheAlaGlnAspTyrAlaLeuIleSerLeuGlnAlaHisThrMetTyrG 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        151 GCACTGAAGCTTGGGGGCCAAAAAGGTGTTCATTGAGGATGTCAGCAGGGA 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51 AlaLeuGluValGlyAlaThrAsnSerTyrValIleAspAlaLysGluGl 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      101 ATCTGGCCAACATTGGCCAGAAGGAAGACTTCGAGGAAGCCAGGAAGAAG 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34 ysCysLeuAspValGiyGluGlyLysAspLeuAlaPheValGlnGlnLys 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17 rSerValAlaTleLysTrpLeuGlnGluGlnGlyTyrAsnValIleAlac 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51 CTCGTGCATCCTCGTGTGGCTGAAGGAACAAGGCTATGACGTCATTGCCT 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quality:
Ratio:
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seq_documentation_block:
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial correct a license agreement (See http://www.isb-slb.ch/announce/
                                                                                                                           MEDIINE-20445173; PubMed=10993077;
Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.;
"Genome sequence of the endocellular bacterial symbiont of aphids buchners ap, Aps.",
Nature 407:81-86(2000).
-! CATALYTIC ACTIVITY: ATP + L-CITRULLINE + L-ASPARTATE = AMP + PYROPHOSPHATE + L-RAGININOSUCCINATE.
-! PATHWAY: PENULTIMATE STEP IN ARGININE BIOSYNTHESIS.
-! SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                       Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum Symbiotic bacterium).
Bacteria; Proteobacteria; gamma subdivision; Buchnera.
                                                                                                                                                                                                                                                                                                                       STRAIN-TOKYO 1998;
                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                   20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
ARGININOSUCCINATE SYNTHASE (EC 6.3.4.5) (CITRULLINE--ASPARTATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1151 AGCCAACTGATGCCACCGGGTTCATCAACATCAATTCCCTCAGGCTGAAG 1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1101 GTCTCTCTACAATGAGGAGCTGGTGAGCATGAACGTGCAGGGTGATTATG 1150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ASSY_BUCAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    374 spHisHisAlaAlaTleGlyPheTleGluLeuTrpGlyLeuProThrLys 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1051 GTGTCCGTCCTCAAGGGCCAGGTGTACATCCTCGGCCGGGAGTCCCCACT 1100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  357 rSerLeuTyrAspGluLysLeuAlaThrTyrThrLysAspAspAlaPheA 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1001 TCCGCCACTGCATCGCCAAGTCCCAGGAGCGAGTGGAAGGGAAAGTGCAG 1050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                341 ValLysLeupheLysGlyHisAlaIleValGluGlyArgLysSerGluTy 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            324 euHisAlaPheLeuLysGluThrGlnLysHisValThrGlyTleValArg 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          307 tSerGluIleTleTyrAsnGlyLeuTrpPheSerProLeuLysAspAlaL 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          951 TGCTGAGCTGGTGTATACCGGTTTACGGCCTAGCCCTGAGTGTGAATTTG 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         291 ThrLeuValLysGluValAlaHisPheLysProIleIleGluGlnLysMe 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       901 ACCATGGACCGGGAAGTGCGCAAAATCAAACAAGGCCTGGGCTTGAAATT 950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      274 ysproGlyAlaMetThrLeuIleLysAlaHisLysGluLeuGluAspLeu 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    851 CCCCAGCAGGCACCATCCTTTACCATGCTCATTTAGACATCGAGGCCTTC 900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     257 pHisValGluAsnArgLeuValGlyIleLysSerArgGluValTyrGluC 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     801 CATCGTGGAGAACCGCTTCATTGGAATGAAGTCCCGAGGTATCTACGAGA 850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
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SQ SQ
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US-09-775-693-1 x ASSY_BUCAI
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PROSITE; PS00564; ARGININOSUCCIN_SYN_1; 1.

PROSITE; PS00565; ARGININOSUCCIN_SYN_2; 1.

Arginine biosynthesis; Ligase; ATP-binding; Complete proteome.

SEQUENCE 403 AA; 45072 MW; F23B7024C8BDB147 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        116 GCCAG...AAGGAAGACTTCGAGGAAGCCAGGAAGAAGGCACTGAAGCTT 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         163 GGGGCCAAAAAGGTGTTCATTGAGGATGTCAGCAGGGAGTTTGTGGAGGA 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 213 GTTCATCTGGCCGGCCATCCAGTCCAGCGCACTGTATGAGGACCGCTACC 262
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69 GCTGAAGGAACAA...GGCTATGACGTCATTGCCTATCTGGCCCAACATTG 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                      413 AGATAAAGGTCATTGCTCCCTGGAGGATGCCTGAATTCTACAACCGGTTC 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               125 sGlyAsnAspGlnValArgPheGluMetAlaTyrAlaAlaLeuAlaProA 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    363 GGGGAACGATCAGGTCCGGTTTGAGCTCAGCTGCTACTCACTGGCCCCCC 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   313 ATCGCCCAGCGGAGGGGGCCAAGTATGTGTCCCACGGCGCCACAGGAAA 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  263 TCCTGGGCACCTCTTGCCAGGCCCTGCATCGCCCGCAAACAAGTGGAA 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |||||||::::::: |||||:::::::||||||::::|||||:::
59 GlyAlaSerSerCysHisValPheAspLeuLysGluGluPheIleGluAs 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 42 lyGlnSerLysLysAspLeuAsnGlyIleGluLysLysSerLeuGluSer 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25 pLeuLysGluAsnTyrAsnPheGluValValAlaPheValAlaAspIleG 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            75 nTyrValTyrProValLeuLysThrGlyAlaLeuTyrGluGlySerTyrL 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        142 snLeuAsnValIleAlaProTrpArg.....GluTrp.....AsnLeu 154
                                                                                                                                                                                                                                                                                                                                                                463 AAGGGCCGCAATGACCTGATGGAGTACGCAAAGCAACACGGGATTCCCCAT 512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92 euLeuGlyThrAlaMetAlaArgProIleIleAlaLysLysGlnValGlu 108
                                                                                                                                                                                         563 TCAGCTACGAGGCTGGAATCCTGGAGAACCCAAGAACCAAGCGCCTCCA 612
                                                                                                                                                                                                                                   171 rThrAlaThrLeuGluLysIleTyrSerLysAspGluAsnSerTrpHisI 188
                                                                                                                                                                                                                                                                          513 CCCGGTCACTCCCAAGAACCCGTGGAGCATGGATGAGAACCTCATGCACA 562
                                                                                                                                                                                                                                                                                                                      155 AsnSerArgGluSerLeuLeuLysTyrLeuAspLysLysAsnIleSerTh 171
                                                                                                   613 GGTCTCTACACGAAGACCCAGGACCCAGCCAAAGCCCCCAACACCCCTGA 662
                663 CATTCTCGAGATCGAGTTCAAAAAAGGGGTCCCTGTGAAGGTGACCAACG 712
                                                            205 AspCysTrpSerTrpThrValAsnProGluAspAlaProGluLysProGl 221
                                                                                                                                               leSerThrGluGlyGlyLeuLeuGluAsnProTrpAsnGlnSerAsnGlu 204
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807.50
2.710
75.253
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seq_name: SwissProt_39:ASSY_AQUAE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    221 uTyrValSerLeuGlnLeuLysGluGlyCysValValSerValAsnAsnG 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               238 lnLys.....LeuAsnProLeuLysCysValGluGluLeu 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1113 TGAGGAGCTGGTGAGCATGAACGTGCAGGGTGATTATGAGCCAACTGATG 1162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   333 laAspSerLeuSerLeuGluIleThrGlyGluValIleLeuLysLeuTyr 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                350 LysGlyServalThrAlaValGlnLysLysSerProAsnSerLeuTyrSe 366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           383 laAspGlyPheIleArgLeuPheSerLeuSerSerLys 395
                                                                                                                                                                                                                                                                                                                   Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L., Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Huber Feldman R.A., Short J.M., Olson G.J., Swanson R.V., "The complete genome of the hyperthermophilic bacterium Aquifex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Aquificales; Aquificaceae; Aquifex
                                                                     NATURE 392:353-358(1998).

NATURE 392:353-358(1998).

I CATALYTIC ACTIVITY: ATP + L-CITRULLINE + L-ASPARTATE = AMP + 1 CATALYTIC ACTIVITY: ATP + L-CITRULLINE + L-ASPARTATE.

PYROPHOSPHATE + L-ARGININOSUCCINATE.

PATHWAY: PENULTIMATE STEP IN ARGININOSUCCINATE SYNTHASE FAMILY.

SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=98196666; PubMed=9537320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=63363;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Aquifex aeolicus.
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This SWISS-PROT entry is copyright. It is produced through a collaboration
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alignment_block:
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           560 ACATCAGCTACGAGGCTGGAATCCTGGAGAACCCAAGAACCAAGCGCCCT 609
                                               165 oVallysAlaThrLysGluLysProTyrSerIleAspArgAsnLeuTrpG 182
                                                                                            510 CATCCCGGTCACTCCCAAGAACCCGTGGAGCATGGATGAGAACCTCATGC 559
                                                                                                                                                                 460 TTCAAGGGCCGCAATGACCTGATGGAGTACGCAAAGCAACACGGGATTCC 509
                                                                                                                                     149 PheLysSerArgGluGluGlnValGluTyrAlaGlnArgPheAsnilePr 165
                                                                                                                                                                                                                     136 roAspileGluValLeuAlaProValArgGluTrpGlu...... 148
                                                                                                                                                                                                                                                                410 CCCAGATAAAGGTCATTGCTCCCTGGAGGATGCCTGAATTCTACAACCGG 459
                                                                                                                                                                                                                                                                                                         119 yLysGlyAsnAspGlnValArgPheGluLeuSerValTrpAlaLeuAsnP 136
                                                                                                                                                                                                                                                                                                                                               360 AAAGGGGAACGATCAGGTCCGGTTTGAGCTCAGCTGCTACTCACTGGCCC 409
                                                                                                                                                                                                                                                                                                                                                                                        103 TyrTyrAlaGluLysPheAsnAlaAspTyrValAlaHisGlySerThrGl 119
                                                                                                                                                                                                                                                                                                                                                                                                                                 310 GAAATCGCCCAGCGGGAGGGGGCCAAGTATGTGTCCCACGGCGCCCACAGG 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     260 ACCTCCTGGGCACCTCTCTTGCCAGGCCCTGCATCGCCCGCAAACAAGTG 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      210 GGAGTTCATCTGGCCGGCCATCCAGTCCAGCGCACTGTATGAGGACCGCT 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        160 CTTGGGGCCAAAAAGGTGTTCATTGAGGATGTCAGCAGGGAGTTTGTGGA 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          86 yrProLeuThrAlaAlaLeuSerArgProLeuIleAlaGluArgLeuVal 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          110 ACATTGGCCAGAAGGAAGACTTCGAGGAAGCCAGGAAGAAGGCCACTGAAG 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              69 uAsnTyrCysLeuProThrLeuArgAlaLeuAlaLeuTyrGluGlyLysT 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             53 AlaGiyAiaTleGluAlaTleValGluAspLeuLysGluThrPheAlaGl 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PP00764; Arginosuc_synth; 1.
ProDom; PD003544; Arginosuc_synth; 1.
PROSITE; PS00564; ARGININOSUCCIN_SYN_1; 1.
PROSITE; PS00565; ARGININOSUCCIN_SYN_2; 1.
Arginine biosynthesis; Ligase; ATP-binding; Complete proteome.
SEQUENCE 401 AA; 45848 MW; 2BCBA9D027CE33CF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36 spValGlyGlnGlyGluGluLeuSerGluIleProGluLysAlaArgArg 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19 eValArgTrpLeuThrGluLysGlyTyrGluValIleThrTyrThrAlaA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60 CCTCGTGTGGCTGAAGGAACAAGGCTATGACGTCATTGCCTATCTGGCCA 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10 AAAGGCTCCGTGGTTCTGGCCTACAGTGGCGGCCTGGACACCTCGTGCAT 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AE000725; AAC07170.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 LysLysArgVailleLeuAlaTyrSerGlyGlyLeuAspThrSerIleIl 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Quality:
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111:::111
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2.741
72.277
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20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
ARGININOSUCCINATE SYNTHASE (EC 6.3.4.5) (CITRULLINE--ASPARTATE
                                                                                                                     Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
                                                                                                                                                                                                    ARGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1207 CATCGTCTCCAG 1218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1157 CTGATGCCACCGGGTTCATCAACATCAATTCCCTCAGGCTGAAGGAATAT 1206
                                                                                                    NCBI_TaxID=1360;
                                                                                                                                              Lactococcus lactis (subsp. lactis) (Streptococcus lactis)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1107 CTACAATGAGGAGCTGGTGAGCATGAACGTGCAGGGTGATTATGAGCCAA 1156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   395 GlyArgValArg 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     378 leAlaGlyLysHisPheThrLysValTrpGlyLeuProLeuLysValLeu 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1057 GTCCTCAAGGGCCAGGTGTACATCCTCGGCCGGGAGTCCCCACTGTCTCT 1106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1007 ACTGCATCGCCAAGTCCCAGGAGCGAGTGGAAAGGGAAAGTGCAGGTGTCC 1056
                                                                                                                                                                                                                                                                                                                                                       ASSY_LACLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             361 uTyrValGluGluLeuAlaThrTyrSerGluLysAspGlnPheAspGlnI 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        345 LeuTyrLysGlySerValSerValGlyArgArgSerProAsnSerLe 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              328 laPheThrAsnLysIleAlaGluPheAlaThrGlyGluVaiArgLeuLys 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      311 sLeuValTyrGluGlyLeuTrpPheThrProLeuArgGluAlaLeuAspA 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   957 GCTGGTGTATACCGGTTTACGGCCTAGCCCTGAGTGTGAATTTGTCCGCC 1006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               295 ArgPheThrPheHisTyrPheLeuThrHisIleProHisGluTyrAlaLy 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           910 CGG...GAAGTGCGCAAAATCAAACAAGGCCTGGGCTTGAAATTTGCTGA 956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  278 laMetValLeuTyrGluAlaTyrArgAspLeuLeuSerLeuValLeuAsp 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   860 GCACCATCCTTTACCATGCTCATTTAGACATCGAGGCCTTCACCATGGAC 909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             261 uAsnArgLeuValGlyIleLysSerArgGluIleTyrGluAlaProGlyA 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        810 GAACCGCTTCATTGGAATGAAGTCCCGAGGTATCTACGAGACCCCAGCAG 859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     245 LeuAsnGluIleAlaGlyArgHisGlyValGlyArgIleAspMetValGl 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 760 CTGAACGAAGTCGCGGCAAGCATGGCGTGGGCCGTATTGACATCGTGGA 809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              231 ......AsnGlyGluArgTyrGluGluGlnTrpLysLeuIleAlaAsn 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          710 ACGTCAAGGATGGCACCACCCACCAGACCTCCTTGGAGCTCTTCATGTAC 759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   215 oGluTyrValThrValGlyPheGluLysGlyLysProValTyrLeu.... 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                660 TGACATTCTCGAGATCGAGTTCAAAAAAAGGGGTCCCTGTGAAGGTGACCA 709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              199 GlnAspAlaTyrGlnIleThrGlnSerProGluGluAlaProAspGluPr 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          610 CCAGGTCTCTACACGAAGACCCAGGACCCAAGCCCAAAGCCCCCAACACCCC 659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      182 lyValSerIleGluCysGlyProLeuGluAspProTrpGlnGluProPro 198
                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                           398 AA
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alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Align seg 1/1 to: ASSY_LACLA from: 1 to: 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-775-693-1 x ASSY_LACLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bolotin A., Wincker P., Mauger S., Jaillon O., Malarme K., Weissenbach J., Ehrlich S.D., Sorokin A.;
"The complete genome sequence of the lactic acid bacterium Lactococcus lactis ssp. lactis II1403.";
Genome Res. 11:731-753(2001).

-i- CATALYTIC ACTIVITY: ATP + L-CITRULLINE + L-ASPARTATE = AMP +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Interpro; IPR001518; Arginosuc_synth.

Pfam; PF00764; Arginosuc_synth; 1.

ProDom; PD003544; Arginosuc_synth; 1.

PROSITE; PS00564; ARGININOSUCCIN_SYN_1; 1.

PROSITE; PS00565; ARGININOSUCCIN_SYN_2; 1.

Arginine biosynthesis; Ligase; ATP-binding; Complete proteome.

SEQUENCE 398 AA; 43960 MW; 11411DF9C9274712 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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-!- PATHWAY: PENULTIMATE STEP IN ARGININE BIOSYNTHESIS.
-!- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the European Bioinformatics Institute. There are no rest use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AE006250; AAK04222.1; -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      101 ATCTGGCCAACATTGGCCAGAAGGAAGACTTCGAGGAAGCCCAGGAAGAAG 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              301 AAACAAGTGGAAATCGCCCAGCGGGGGGGGGCCAAGTATGTGTCCCACGG 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        251 AGGACCGCTACCTCCTGGGCACCTCTCTTGCCAGGCCCTGCATCGCCCGC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                            84 luAsnLysTyrProLeuValSerAlaLeuSerArgProLeuIleAlaGln 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51 AlaLeuGlnValGlyAlaValGluSerValValLeuAspCysLysGluGl 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34 spCysMetAspValGlyGluGlyLysAspLeuAsnPheIleHisAspLys 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17 rSerValAlaValLysTrpLeuThrAspLysGlyPheAspValIleAlaA 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51 CTCGTGCATCCTCGTGTGGCTGAAGGAACAAGGCTATGACGTCATTGCCT 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 metmetGlyAsnLysLysIleValLeuAlaTyrSerGlyGlyLeuAspTh 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ATGTCCAGCAAAGGCTCCGTGGTTCTGGCCTACAGTGGCGGCCTGGACAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation its European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         uPheAlaLysIlePheValGlyAlaAlaLeuLysGlyAsnLeuMetTyrG 84
                                   CACTGGCCCCCAGATAAAGGTCATTGCTCCCTGGAGGATGCCTGAATTC 450
                                                                                                                    yCysThrGlyLysGlyAsnAspGlnValArgPheGluValAlaIleHisS 134
                                                                                                                                                                                                         CGCCACAGGAAAGGGGAACGATCAGGTCCGGTTTGAGCTCAGCTGCTACT 400
                                                                                                                                                                                                                                                                                      {\tt LysLeuValGluValAlaLysGluLysGlyAlaThrAlaIleAlaHisGluysLeuValGluValAlaLysGluLysGlyAlaThrAlaIleAlaHisGluysLeuValGluValAlaLysGluysGlyAlaThrAlaIleAlaHisGluysLeuValGluValAlaLysGluLysGlyAlaThrAlaIleAlaHisGluysLeuValGluValAlaLysGluLysGlyAlaThrAlaIleAlaHisGluysLeuValGluValAlaLysGluLysGlyAlaThrAlaIleAlaHisGluysLeuValGluValAlaHisGluysLeuValGluYalaHisGluysLeuValGluYalaHisGluYalaHisGluysLeuValGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaHisGluYalaH
Quality:
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AC DT DT DT DE DE DE GN

ARGG OR SLR0585

LIGASE)

01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
ARGININOSUCCINATE SYNTHASE (EC 6.3.4.5) (CITRULLINE--ASPARTATE

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seq_documentation_block:

ASSY_SYNY3

STANDARD;

PRT;

400 AA

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134 erLeuAlaProGluLeuGluValIleAlaProValArg......GluTrp 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            551 ACCTCATGCACATCAGCTACGAGGCTGGAATCCTGGAGAACCCCAAGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         501 CGGGATTCCCATCCCGGTCACTCCCAAGAACCCGTGGAGCATGGATGAGA 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              149 His.....TrpAlaArgGluGluIleGluTyrAlaAsnGlnAs 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    451 TACAACCGGTTCAAGGGCCGCAATGACCTGATGGAGTACGCAAAGCAACA 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    162 nGlyValProIleProAlaAspLeuAspAsnProTyrSerIleAspMetA 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 651 CAACACCCCTGACATTCTCGAGATCGAGTTCAAAAAAGGGGTTCCCTGTGA 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      196 ThrCysProGluAspAlaPhePheMetThrAsnSerValGluAsnAlaPr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            601 CAAGCGCCTCCAGGTCTCTACACGAAGACCCAGGACCCAGCCAAAGCCCC 650
                                                                                                                                                               1101 GTCTCTCTACAATGAGGAGCTGGTGAGCATGAACGTGCAGGGTGATTATG 1150
                                                                                                                                                                                                                                                                         1051 GTGTCCGTCCTCAAGGGCCAGGTGTACATCCTCGGCCGGGAGTCCCCACT 1100
                                                                                                                                                                                                                                                                                                                                                                                          1001 TCCGCCACTGCATCGCCAAGTCCCAGGAGCGAGTGGAAGGGAAAGTGCAG 1050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 751 TTCATGTACCTGAACGAAGTCGCGGGCAAGCATGGCGTGGGCCGTATTGA 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    701 AGGTGACCAACGTCAAGGATGGCACCACCACCAGACCTCCTTGGAGCTC 750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               212 oAsnGluAlaGluPheIleGluValGluPheLysGluGlyLeuProIleA 229
                                                     1151 AGCCAACTGATGCCACCGGGTTCATCAACATC 1182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               851 CCCCAGCAGGCACCATCCTTTACCATGCTCATTTAGACATCGAGGCCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            801 CATCGTGGAGAACCGCTTCATTGGAATGAAGTCCCGAGGTATCTACGAGA 850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            229 laLeu...AsnGlyLysSerLeuGluLeuHis......GluIle 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    951 TGCTGAGCTGGTGTATACCGGTTTACGGCCTAGCCCTGAGTGTGAATTTG 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            291 ThrPheValArgGluLeuAlaHisPheLysProValLeuGluAsnGluLe 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          274 ysproAlaAlaIleThrLeuLeuLysAlaHisLysAspLeuGluAspLeu
                                                                                                                                                                                                                    341 IleLysLeuTyrLysGlyLeuAlaThrProValGlyArgLysSerThrAs 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 901 ACCATGGACCGGGAAGTGCGCAAAATCAAACAAGGCCTGGGCTTGAAATT 950
374 spGlnAlaAlaValGlyPheIleLysLeu 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       \tt pHisIleGluAsnArgLeuValGlyIleLysSerArgGluPheTyrGluC
                                                                                                          nSerLeuTyrSerGluLysLeuAlaThrTyrThrAlaAlaAspGluPheA 374
                                                                                                                                                                                                                                                                                                                               euIleAlaTyrLeuAspGluThrGlnLysValValAsnGlyIleValLys 340
                                                                                                                                                                                                                                                                                                                                                                                                                                            uAlaAsnLeuIleTyrAsnGlyLeuTrpPheAsnProAlaThrLysAlaL 324
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alignment_block:
US-09-775-693-1 x ASSY_SYNY3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to: ASSY_SYNY3 from: 1 to: 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
                            245 TGTATGAGGACCGCTACCTCCTGGGCACCTCTCTTGCCAGGCCCTGCATC 294
                                                                                                                       195 CAGGGAGTTTGTGGAGGAGTTCATCTGGCCGGCCATCCAGTCCAGCGCAC 244
                                                                                                                                                                                                        145 AAGAAGGCACTGAAGCTTGGGGCCAAAAAGGTGTTCATTGAGGATGTCAG 194
                 84
                                                                                                  67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Piam; PF00764; Arginosuc_synth; 1.

ProDom; PD003544; Arginosuc_synth; 1.

PROSITE; PS00564; ARGININOSUCCIN_SYN_1; 1.

PROSITE; PS00565; ARGININOSUCCIN_SYN_2; 1.

Arginine biosynthesis; Ligase; ATP-binding; Complete proteome.

SEQUENCE 400 AA; 44485 MW; 37BDB758CBB82C05 CRC64;
                                                                                                                                                                 34 leThrLeuAlaAlaAspLeuGlyGlnGlyAspGluLeuGlyProIleGln 50
                                                                                                                                                                                                                                                                                           95 TTGCCTATCTGGCCAACATTGGCCAGAAGGAAGACTTCGAGGAAGCCAGG 144
                                                                                                                                                                                                                                                                                                                                  17 rSerValCysIleProTyrLeuMetHisGluTrpGlyValGluGluValI 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                         51 CTCG...TGCATCCTCGTGTGGCTGAAGGAACAAGGCTAT...GACGTCA 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; D90917; BAA18841.1; -.
InterPro; IPR001518; Arginosuc_synth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       - CATALYTIC ACTIVITY: ATP + L-CITRULLINE + L-ASPARTATE = AMP + PYROPHOSPHATE + L-ARGININOSUCCINATE.
- PARTHWAY: PENULTIMATE STEP IN ARGININE BIOSYNTHESIS.
- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
- SIMILARITY: BELONGS TO THE ARGININOSUCCINATE SYNTHASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=97061201; PubMed=8905231; Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y., Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T., Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
                                                                                                                                                                                                                                                                                                                                                                                                                   ||||:::
| MetGlyargalaLysLysValValLeualaTyrSerGlyGlyValAspTh
                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ATGTCCAGCAAAGGCTCCGTGGTTCTGGCCTACAGTGGCGGCCTGGACAC 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synechocystis sp. (strain PCC 6803).
Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
                                                                                sGluGluPheValLysGluTyrAlaPheArgSerIleGlnAlaAsnAlaL 84
euTyrGluAsnArgTyrProLeuSerThrAlaLeuAlaArgProLeuIle 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3:109-136(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              69.458
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2.709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             percent Identity: 41.626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length:
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83 AATTCCCTCAGGCTGAAG 1200
, –
.083 CGGCCGGGA :: 353 aGlyArgLy
3 GTGGAAGGGAAAGTO
83 GCCCTGAGTGTGAATTTGTCCGCC.
33 AGGCCTGG : ::: 03 nThrValG
183 TTAGACATCGAGGCCTTCAC
33 CCCGAGGTATCTACGAGACCCCAGCAGGCACCATCCTTT
83 TGGCGTGGGCCGTATTO
33 CAGACCTCCTTGGAGCTCTTCATGTACCTGA
86 AAGGGTCCCTGTGAAGGTGACCAACGTCAAGGATGG ::: ::::::::::: 26 ysGlyIleProValSerLeuAsnGlyValMetLeuAspPr
36 CCCAGCCAAAGCCCCCAACACCC ::: ::: 09 alleAlaAspThrProAspGlu
86 GAGAACCCAAGAACCAAGCGCCTCCAGGTCTCTACACGA :::
36 GGAGCATGGATGAGAACCT :: ::: ::: :: 76 yrSerIleAspArgAsnIl
6 GTACGCAAAGCAACACGGGATTCCCATCCC ::::::::: ::: 9 aTyrGlyGluArgTyrGlyValGluSerPr
6 AGGATGCCTGAATTCTACAACCGGTTCAAGGGCCGCAATGAC::: :::: ::: ::: :::: ::::: 1 LysMet
95 GCTACTCACTGGCCCCCAGATAAAGGTCATTGG::::
145 CCACGG : :17 aHisGly
AAGTGGAAATCGCCCAGCGGGAGGGGGCCAAG9

us-09-775-693-1.rsp

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seq_name: Swissprot_39:ASSY_ARCFU
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                                                                                                                                                                                                                                                                                                                  alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         387 TrpGlyLeuProThrLys 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ASSY_ARCFU
O28032;
                                                                                                                                                                       alignment_block:
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15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
ARGININOSUCCINATE SYNTHASE (EC 6.3.4.5) (CITRULLINE--ASPARTATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-98049343; PubMed-9389475;

MEDLINE-98049343; PubMed-9389475;

Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,

Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,

Klenk H.-P., Clayton R.A., Tomb J.-F., Wprides N.C.,

Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,

Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,

Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.D., Loftus B.,

Reich C.I., Quackenbush J., Lee N.H., Sladms M.D., Loftus B.,

Peterson S. Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou I

Peterson S. Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou I

Peterson S. Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou I

Peterson S. Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou I

Peterson S. Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou I

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Peterson S. Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou I

Peterson S. Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou I

Peterson S. Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou I

Peterson S. Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou I

Peterson S. Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou I

Peterson S. Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou I

Peterson S. Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou I

Peterson S. Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou I

Peterson S. Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou I

Peterson S. Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou I

Peterson S. Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou I

Peterson S. Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou I

Peterson S. Reich 
                                                                                                                                        US-09-775-693-1 x ASSY_ARCFU
                                                                                                                                                                                                                                   Percent Similarity:
                                                                                  Align seg 1/1 to: ASSY_ARCFU from: 1 to: 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Archaeoglobus fulgidus.
Archaeoglobales; Archaeoglobales; Archaeoglobaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way use by non-profit institutions as long as its content is in no way of the statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 390:364-370(1997).
-i- CATALYTIC ACTIVITY: ATP + L-CITRULL.
-i- CATALYTIC ACTIVITY: ATP + L-CITRULL.
-i- CATALYTIC ACTIVITY: ATP + L-CITRULL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The complete genome sequence of the hyperthermophilic, sulphate-
reducing archaeon Archaeoglobus fulgidus.";
                                                                                                                                                                                                                                                                                                                                                                                                           prior, prior64; Arginosuc_synth; 1.
probom; pp003544; Arginosuc_synth; 1.
prosite; ps00564; ARGININOSUCCIN_SYN_1; 1.
pROSITE; ps00565; ARGININOSUCCIN_SYN_2; 1.
prosite; ps00565; ARGININOSUCCIN_SYN_2; 1.
complete proteome.
Arginine biosynthesis; Ligase; ATP-binding; Complete proteome.
SEQUENCE 390 AA; 44104 MW; 31334D84F696EEBD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AE000949; AAB89005.1; -.
                            19 GTGGTTCTGGCCTACAGTGGCGGCCTGGACACCTCGTGCATCCTCGTGTG 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PANHWAY: PENULTIMATE STEP IN ARGININE BIOSYNTHESIS.
SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
SIMILARITY: BELONGS TO THE ARGININOSUCCINATE SYNTHASE FAMILY.
Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IPR001518; Arginosuc_synth.
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                                                                                                                                                                                                                                                750.50
2.544
72.482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATP + L-CITRULLINE + L-ASPARTATE = AMP
                                                                                                                                                                                                                                                Percent Identity: 43.735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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                                                                                                                                                                                                                                                                                                                      Length:
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113 TTGGCCAGAAGGAA...GACTTCGAGGAAGCCAGGAAGAAGGCACTGAAG 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               160 CTTGGGGCCAAAAAGGTGTTCATTGAGGATGTCAGCAGGGAGTTTGTGGA 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              69 GCTGAAGGAACAA...GGCTATGAC...GTCATTGCCTATCTGGCCAACA 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         210 GGAGTTCATCTGGCCGGCCATCCAGTCCAGCGCACTGTATGAGGACCGCT 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19 uLeuLysGluLysTyrGlyPheAspGluVallleThrValThrValAspI 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                260 ACCTCCTGGGCACCTCTCTTGCCAGGCCCTGCATCGCCCGCAAACAAGTG 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36 leGlyGlnProGluAlaAspIleLysGlnAlaGluGluArgGlyLysLys 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100 GluvalalaLysLysGluGiyalaGluAlaValAlaHisGlyCysThrGl 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        310 GAAATCGCCCAGCGGGAGGGGCCAAGTATGTGTCCCCACGGCGCCACAGG 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           53 Tyr...AlaAspLysHisTyrThrIleAspAlaLysLysGluPhevalAs 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 ValValLeuSerTyrSerGlyGlyLeuAspThrThrValCysIleProLe 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     68 pSer...LeuPheMetLeuTleLysAlaAsnGlyAsnTyrGluGly...T 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         410 CCCAG.....ATAAAGGTCATTGCTCCCTGGAGGATGCCTGAATTCTAC 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             116 yLysGlyAsnAspGinLeuArgPheGlu......AsnIlePheA 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  360 AAAGGGGAAGGATCAGGTCCGGTTTGAGCTCAGCTGCTACTCACTGGCCC 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            83 yrValleuGlyThrAlaLeuAlaArgProLeuIleAlaGluLySValVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           504 GATTCCCATCCCGGTCACTCCCAAGAACCCGTGGAAGCATGGATGAGAACC 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               454 AACCGGTTCAAGGGCCGCAATGACCTGATGGAGTACGCAAAGCAACACGG 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       129 rgGlnHisGlyPheLysValileAlaProValArgGluLeuAsnLeuThr 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      157 yIleGluValProAlaThrLysGluLysProTyrSerIleAspGluAsnL 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            604 GCGCCTCCAGGTCTCTACACGAAGACCCAGGACCCAGGCCAAAGCCCCCAA 653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                174 euTrpSerArgSerValGluGlyGlyLysLeuGluAspProSerPheGlu 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    554 TCATGCACATCAGCTACGAGGCTGGAATCCTGGAGAACCCCAAGAACCAA 603
                                                                                                                                                                                                                                                                                                                                                                 654 CACCCCTGACATTCTCGAGATCGACTTCAAAAAAAGGGGTCCCTGTGAAGG 703
                                                                                                                                                                                                                                                                                                                                                                                                                                          191 ProProGluAspIleTyrGluTrpThrAlaSerProGluLysAlaProAs 207
                                                                                                                                                                                                                     754 ATGTACCTGAACGAAGTCGCGGGCAAGCATGGCGTGGGCCGTATTGACAT 803
                                                                                                                                                                                                                                                                                           224 euAsnAspGluArgMetGly.......GlyPheGluLeuIle 235
                                                                                                                                                                                                                                                                                                                               704 TGACCAACGTCAAGGATGGCACCACCACCAGACCTCCTTGGAGCTCTTC 753
                                                                                                                                                                                  804 CGTGGAGAACCGCTTCATTGGAATGAAGTCCCGAGGTATCTACGAGACCC 853
                                                                                                          854 CAGCAGGCACCATCCTTTACCATGCTCATTTAGACATCGAGGCCTTCACC 903
                                                                                                                                          252 tIleGluAspArgValLeuGlyLeuLysAlaArgGluAsnTyrGluHisP 269
                                                                          269 roAlaAlaThrIleLeuIleThrAlaHisArgAspLeuGluAsnLeuVal
286 LeuSerArgGluLeuLysPheLysLysPheValGluGluGluTrpAl 302
                                    904 ATGGACCGGGAAGTGCGCAAAATCAAACAAGGCCTGGGCTTGAAATTTGC 953
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seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_name: SwissProt_39:ASSY_METJA
                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
Pfam; PF00764; Arginosuc_synth; 1.
                                            interPro;
                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-JAL-1 / D.M. 2661 / ATCC 43067;

MEDLINE-9637999; PubMed-8688087;

Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,

Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,

Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,

Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,

Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.C.,

"Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                        EMBL; U67494; AAB98414.1; -.
TIGR; MJ0429; -.
                                                                                                                                                                                                                                                                 -!- PATHWAY: PENULTIMATE STEP IN ARGININE BIOSYNTHESIS.
-!- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE ARGININOSUCCINATE SYNTHASE FAMILY.
                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
ARGININOSUCCINATE SYNTHASE (EC 6.3.4.5) (CITRULLINE--ASPARTATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1195 CTGAAGGAATATCATCGTCTC 1215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=2190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Methanococcus jannaschii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1154 CAACTGAT......GCCACCGGGTTCATCAACATCAATTCCCTCAGG 1194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ARGG OR MJ0429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1104 TCTCTACAATGAGGAGCTGGTGAGCATGAACGTGCAGGGTGATTATGAGC 1153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           382 GlyArgLeuPheArgArgLeu 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1054 TCCGTCCTCAAGGGCCAGGTGTACATCCTCGGCCGGGAGTCCCCACTGTC 1103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ASSY_METJA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  365 erileAspGlnArgLeuAlaGluGLyPheAlaAlaPheHisGlyLeuGln 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1004 GCCACTGCATCGCCAAGTCCCAGGAGCGAGTGGAAGGGAAAGTGCAGGTG 1053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      352 aLeuTyrSerGluGluLeuValSerPhe......AspThrGluS 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              336 LysLeuTyrLysGlySerAlaValValValAlaArgAsnSerProTyrAl 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    319 snAlaPheIleAspLysThrGlnGluArgValThrGlyTrpValLysVal 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          302 aGluLeuvalTyrTyrGlyLeuValAsnAspProLeuPheAspAlaLeuA 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     954 TGAGCTGGTGTATACCGGTTTACGGCCCTAGCCCTGAGTGTGAATTTGTCC 1003
                      IPR001518; Arginosuc_synth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
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alignment_block:
US-09-775-693-1 x ASSY_METJA
214 eValGiurieGlupheLysGluGlyValProValAlaTleAsnGlyGluL 231
                   666 TCTCGAGATCGAGTTCAAAAAAGGGGTCCCTGTGAAGGTGACCAACCGTCA 715
                                                                         199 IleTyrAlaTrpThrLysAsnProValGlu...AspLysGluGluGluIi 214
                                                                                                                   616 CTCTACACGAAGACCCAGGACCCAGCCAAAGCCCCCAACACCCCCTGACAT 665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Align seg 1/1 to: ASSY_METJA from: 1 to: 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_scores:
                                                                                                                                                       182 errleGluGlySerGluLeuGluAsnProAspPheValProProGluGlu 198
                                                                                                                                                                                               566 GCTACGAGGCTGGAATCCTGGAGAACCCCAAGAACCAAGCGCCTCCCAGGT 615
                                                                                                                                                                                                                                                         516 GGTCACTCCCAAGAACCCGTGGAGGAGGATGGAGAACCTCATGCACATCA 565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quality: 747.00
Ratio: 2.630
Percent Similarity: 70.647
                                                                                                                                                                                                                                   166 o...ThrGluSerLysLysTyrSerIleAspGluAsnLeuTrpGlyArgS 182
                                                                                                                                                                                                                                                                                                                  150 ThrargalaGluGluIleGluTyralaLysGluLysGlyIleProIlePr 166
                                                                                                                                                                                                                                                                                                                                                       466 GGCCGCAATGACCTGATGGAGTACGCAAAGCAACACGGGATTCCCATCCC 515
                                                                                                                                                                                                                                                                                                                                                                                         138 euLysIleIleAlaProIleArg.....AspLeuAsnLeu 149
                                                                                                                                                                                                                                                                                                                                                                                                                          416 TAAAGGTCATTGCTCCCTGGAGGATGCCTGAATTCTACAACCGGTTCAAG 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 yasnaspGlnPheArgPheGluThrThrIleArgIleLysAlaProHisL 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    366 GAACGATCAGGTCCGGTTTGAGCTCAGCTGCTACTCACTGGCCCCCAGA 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      105 AlaGluGluValGlyAlaGluAlaValAlaHiSGlyCysThrGlyLySG1 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             316 GCCCAGCGGGAGGGGCCAAGTATGTGTCCCCACGGCGCCACAGGAAAGGG 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           266 TGGGCACCTCTCTTGCCAGGCCCTGCATCGCCCGCAAACAAGTGGAAATC 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       216 CATCTGGCCGGCCATCCAGTCCAGCGCACTGTATGAGGACCGCTACCTCC 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    88 euSerThrAlaLeuAlaArgProLeuIleAlaHisLysValValGluIle 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     166 GCCAAAAAGGTGTTCATTGAGGATGTCAGCAGGAGTTTGTGGAGGAGTT 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                72 rīlePheArgĀlaileLysAlaAsnĀlāMetTyrGluGly...TyrProL 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 119 AG...AAGGAAGACTTCGAGGAAGCCAGGAAGAAGGCACTGAAGCTTGGG 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              56 ValLeuLysHisTyrThrIleAspAlaLysGluGluPheValLysAspTy 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          39 inProGluGluGluIleLysGluValGluGluLysAlaLysLysLeuGly 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22 uGluaspLysTyrGlyTyrLysValValSerValCysValAspValGlyG 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           72 GAAGGAACAA...GGCTATGACGTCATTGCCTATCTGGCCAACATTGGCC 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22 GTTCTGGCCTACAGTGGCGGCCTGGACACCTCGTGCATCCTCGTGTGGCT 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ProDom; PD003544; Arginosuc_synth; 1.
PROSITE; PS00564; ARGININOSUCCIN_SYN_1; 1.
PROSITE; PS00565; ARGININOSUCCIN_SYN_2; 1.
Arginine biosynthesis; Ligase; ATP-binding; Complete proteome.
SEQUENCE 395 AA; 44723 MW; 655D4A7AC06E7A7F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 ValLeuAlaTyrSerGlyGlyLeuAspThrSerCysCysLeuLysLeuLe 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Quality:
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CGGCGACTGCACTCC CGGCGACTCCACTCC CGGCACTCCACTC	1166 CCGGGTTCATCAACATCAAFTCCCTCAGGCTGAAGGAATATCATCGTCTC :: ::::: :: :::::::::::::::::::	1116 GGAGCTGGTGAGCATGAACGTGCAGGGTGATTATGAGCCAACTGATGCCA 	1066 GGCCAGGTGTACATCCTCGGCCGGGAGTCCCCACTGTCTCTACAATGA ::: :::::: ::: :::	1016 CCAAGTCCCAGGAGCGAGTGGAAGGGAAAGTGCAGGTGTCCGTCAAG :::	966 TACCGGTTTACGGGCTAGGCCTGAGTGTGAATTTGTCCGCCACTGCATCG	916 GTGCGCAAAATCAAACAAGGCCTGGGCTTGAAATTTGCTGAGCTGGTGTA ::::::: ::: 293 GluLeuArgPheLysGluIleValAspScrLeuTyrGlyGluLeuIleTy	866 TCCTTTACCATGCTCATTTAGACATCGAGGCCTTCACCATGGACCGGGAACCGGGAACCGGGAACCGGGAACCGGGAACCGGGAACCGGGAGCCTTCACCATGGACCGGAACCGGAACCGAACCGAGGACCGAACCGAACCAACACAACA	816 CTTCATTGGAATGAAGTCCCGAGGTATCTACGAGACCCCAGCAGGCACCA ::: :::	766 GAAGTCGCGGGCAAGCATGGCGTGGGCCGTATTGACATCGTGGAGAACCG :::	716 AGGATGGCACCACCACCACCACCTTGGACCTCTTCATCTTACCTGACCTCGACCTCGACCTCGACCTCGACCTCGACCTCGACCTGACACTGACACTGACACTGACACTGACACTGACACTACTGACACTACTGACACTACTGACACTACTACACTACACTACACACTACTACACTACACACTACT
	ATTCCCTCAGGCTGAAGGAATATCATCGTCTC ::::	GGTGCAGGGTGATTATGAGCCAACTGAT ::: :::::::::::::::::::::::::::::::	GGCGGGAGTCCCCACTGTCTCTCTACA ::: 31yArgAspSerProTyrAlaLeuTyrS	rGGAAGGGAAAGTGCAGGTGTCCGTCCT 	CCTGAGTGTGAATTTGTCCGCCACTGC ::: ProLeuArgGluAspLeuAspAlaPhe	GCCTGGGCTTGAAATTTGCTGAGCTGG ;;; ;hihihi; ;LeValAspSerLeuTyrGlyGluLeuI	AGACATCGAGGCCTTCACCATGGACCG(::: ::::::: :salaLeuGluGlnLeuValLeuThrAr	CGAGGTATCTACGAGACCCCAGCAGGC/ 	GCGTGGGCCGTATTGACATCGTGGAGA/ 	uGluProValGluLeuIleLysLysAla

e, *	

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OM of: US-09-775-693-1 to: SPTREMBL_17:* out_format: pfs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                About: Results were produced by the Gencore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Date: Feb 12, 2002 4:10 PM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Command line parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ommanu Lile Farametocci. DEV=xlp
-MODEL=framet_n2p.model -DEV=xlp
-MODEL=framet_n2p.model -DEV=xlp
-Q-Cgn2_1/USPTO_Spool/VS09775693/runat_12022002_124153_1440/app_query.fasta_1.1315
-Q-Cgn2_1/USPTO_Spool/VS09775693/runat_12022002_12.000
-Q-Cgn2_1/USPTO_Spool/VS09775693/runat_12000
-DB=SPTREMBL_17 -OPMT=fastan -SUFFIX=rSD0 -LOOPEXT=0.000
-GAPOT=4.000 -MINMATCH=0.100 -LOOPEXT=0.000 -GAPEXT=0.500
-QGAPOT=6.000 -QGAPEXT=0.000 -YGAPOP=10.000 -YGAPEXT=0.500
-GGAPOT=6.000 -GAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
-FGAPOT=6.000 -DELEXT=7.000 -YGAPOT=10.000 -THR_SCORE=pct
-DELOT=6.000 -DELEXT=7.000 -SPART=1 -MATRIX=bloosum62
-TRANS=human40.cd1 -LIFA-5 -DOCALIGN=200 -THR_SCORE=pct
-TRANS=human40.cd1 -LIFA-MIN-0 -ALIGN=15 -MODEL-LOCAL -OUTFNT=pfs
-TRANS=100 -THR_MIN-0 -MAXLEN=200000000
-NORM=ext -MINLEN=0 -MAXLEN=200000000
-NORM=ext -MINLEN=0 -MAXLEN=200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query: US-09-775-693-1
Query length: 1239
Database: SPTREMBL_17:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Database: SPTREMBL_17:*
Database sequences: 473505
Database length: 146272329
Database length: 146272329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Search information block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Search time (sec): 125.310000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sp_bacteria:Q9RWJ4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sp_bacteria:Q9x2A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sp_bacteria:Q9K4Z3
sp_bacteria:Q9K4Z3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sp_bacteria:Q9PHK7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sp_bacteria:Q9K4Y8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sp_plant:Q9SZX3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sp_archea:Q9UX31
sp_human:O43348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sp_bacteria:Q9KNT8
                                                                                                                                                                                                                                                                                                                                                                                                                                                 sp_bacteria:09JWM1
sp_bacteria:09FC47
sp_bacteria:09PEM9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sp_bacteria:Q9JXC1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sp_archea:Q9HMQ2
                                                                                                                                                                                                                                                                                                                                                                          sp_bacteria:Q9F8M0
sp_bacteria:Q9KHB9
                                                                                                                                                                                                                                                                                                                                                                                                                           sp_archea:Q9V2Z3
                                                                                                                                                                                                                                                                           sp_plant:Q9SDM2
sp_human:Q9C0J8
                                                                                                                                                                                                                                                                                                                                                    sp_virus:0905K9
                                                                                                                                                                                                                                                  sp_plant:004210
                                                                                                                                                                                                                                                                                                                                 sp_human:Q9UF83
                                                                                                                                                        sp_invertebrate:09BKV7 +
sp_vertebrate:057591 + 1
                                                                                                                                                                                                                               sp_plant:09SDM3
                                                                                                       sp_human:Q9NTQ6
sp_plant:Q9M7I5
                                                                                                                                                                                                         sp_human:Q9UFS5
                                                           sp_bacteria:Q9RV01
sp_human:O94850
        sp_rodent:Q9CTW8
                                sp_human:099621
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Strd Orig Zscore
11 + 1026.50 1443.71
14 + 1034.00 1216.81
14 + 948.50 1115.84
14 + 948.50 1115.13
14 + 927.50 1049.24
17 + 885.00 1049.24
18 + 815.00 956.64
18 + 776.00 912.46
18 + 776.100 894.83
17 + 751.50 805.82
10 + 685.50 771.47
1 + 604.50 717.91
1 + 417.50 488.73
11 + 417.50 488.73
                                                                                 + 153.00
149.00 1
148.50 1
146.00 1
142.00 1
                                                                                                                                                                                                                            159.50
157.00
156.50
155.50
153.00
                                                                                                                                                                                                                                                                                                                                                                                                     298.
251.
181.
                                      165.71

165.77
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179.69
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9.4e-73 40

4.2e-60 40

1.7e-54 40
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3.7e-43
3.6e-42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8.9e-51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5.3e-49
                                                                                                                                                                                                                                                                                        1.3e-19
2.1e-19
1.3e-16
2.6e-16
2.6e-16
7.9e-12
9.7e-09
0.0034
0.0037
0.0037
0.0037
0.0198
0.0198
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0.0604
0.0871
0.1623
0.1771
0.2371
0.2155
0.2335
0.2555
                                                                                                                                                                                            0.0434
                                                                                                                                                                                                                                          0.0307
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.3e-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ! Documentation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 opswal thermotoga maritima. arg 109rwid deinococcus radiodurans. 109rwid deinococcus radiodurans. 109hy84 pseudomonas aeruginosa. 109hy84 pseudomonas aeruginosa. 109hk7 campylobacter jejuni. arg 109k820 bacillus halodurans. arg 109k820 bacillus halodurans. arg 109k423 moritella sp. 2674. arg 109sax3 arabidopsis thaliana (mg 109sax3 arabidopsis thaliana arg 109k428 moritella sp. 2693. arg 109k428 moritella sp. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 029262 sus scrofa (pig).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9cc10 mycobacterium leprae. at Q9cc10 mycobacterium leprae. 200x31 sulfolobus solfataricus. Q9ux31 sulfolobus solfataricus. 043348 homo sapiens (human). hy Q43348 halobacterium sp. (strai Q9hmq2 halobacterium sp. (strai
          1 Q99621 homo sapiens (human).
1 Q9ctw8 mus musculus (mouse).
1 Q68872 myxococcus xanthus. hyl
1 Q69895 homo sapiens (human).
                                                                                                       1 057591 fugu rubripes (japanese ji 057591 fugu rubripes (human). hy 1 09ntq6 homo sapiens (human). hj 1 09ntq5 zea mays (maize). arabin 09nv15 zea mays (maize) arabidurans 1 09rv01 deinococcus radiodurans 1 09rv01 deinococcus rhuman). ki 1 094850 homo sapiens (human). ki
                                                                                                                                                                                                                                                                                                                                                                                                                                                 0994wml neisseria meningitidis (
Q9fc47 streptomyces coelicolor
Q9fc47 streptomyces coelicolor
Q9pem9 xylella fastidiosa. argi
Q9v2z3 methanobacterium thermoa
Q9f8m0 carboxydothermus hydroge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q29262 sus scrofa (pig), arginin
Q91xc1 neisseria meningitidis (
                                                                                                                                                                                                                                                                                                                                                    Q9q5k9 herpesvirus papio. ntr
Q9uf83 homo sapiens (human). hy
Q9sdm2 triticum aestivum (wheat
                                                                                                                                                                                                                                                                                                      004210 arabidopsis thaliana (n
                                                                                                                                                                                                                                                                                                                                                                                                                              09khb9 erwinia chrysanthemi
                                                                                                                                                                                                                               Q9ufs5 homo sapiens (human).
                                                                                                                                                                                                                                                                                Q9sdm3 triticum aestivum (wheat
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sp_human:Q99495

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ppq
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OPERATION_block:

prediction_block:

prediction_block:

prediction_block:

prediction_block:

prediction_clock:

prediction
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sp_human:Q9UQ40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sp_rodent:062105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sp_human:Q9UHA8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sp_virus:Q9DWH3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_name: sp_bacteria:Q9X2A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RX MEDILINE-99287316; pubMed=10360571;
RX MEDILINE-99287316; pubMed=10360571;
RA MEDILINE-99287316; pubMed=10360571;
RA Melson K.E., Clayton R.A., Gill S.R., Nelson W.C., Ketchum K.A.,
RA Melson K.E., Clayton R.A., Balek J.A., Linher K.D., Garrett M.M.,
RA McDonald L., Utterback T.R., Malek J.A., Linher K.D., Richardson D.,
RA McDonald L., Cotton M.D., Pratt M.S., phillips C.A., Richardson D.,
RA Stewart A.M., Cotton M.D., Pratt M.S., phillips C.A., White O.,
RA Heidelberg J., Sutton G.G., Venter J.C., Fraser C.M.;
RA Heidelberg J., Smith H.O., Venter J.C., Fraser C.M.;
RA Heidelberg J., Smith H.O., Venter J.C., Fraser C.M.;
RA Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
RT "Evidence for lateral gene transfer between Archaea and Bacteria from
RA Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
RT "Evidence for lateral gene transfer between Archaea and Bacteria from
RA Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
RT "Evidence for lateral gene transfer between Archaea and Bacteria from
RA Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
RT "Evidence for lateral gene transfer between Archaea and Bacteria from
RA Nature 393:323-329(1999)
RT L. CITRULLINE + L-ASPARTATE = AMP +
PYROPHOSPHATE + L-ARGININOSUCCINATE.
C. PYROPHOSPHATE + L-ARGININOSUCCINATE.
C. PYROPHOSPHATE + L-ARGININOSUCCINATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 17, Last annotation update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
ARGININOSUCCINATE SYNTHASE (EC 6.3.4.5) (CITRULLINE--ASPARTATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     percent similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-775-693-1 x Q9X2A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1 to: Q9x2Al from: 1 to: 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pfam; pF00764; Arginosuc_synth; 1.
proDom; pD003544; Arginosuc_synth; 1.
pROSITE; pS00564; ARGININOSUCCIN_SYN_1; 1.
pROSITE; pS00565; ARGININOSUCCIN_SYN_2; 1.
pROSITE; pS00565; ARGININOSUCCIN_SYN_2; 1.
pROSITE; pS00565; ARGININOSUCCIN_SYN_2; 1.
prositional property of the protection of the protectio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- PATHWAY: UREA CYCLE, PENULTIMATE STEP OF THE ARGININE BIOSYNTHETIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001518; Arginosuc_synth.
                                                                 110 ACATTGGCCAGAAGGAAGACTTCGAGGAAGCCAGGAAGAAGGCACTGAAG 159
                                                                                                                                                                                                                                                                                                                                                                                     10 AAAGGCTCCGTGGTTCTGGCCTACAGTGGCGGCCTGGACACCTCGTGCAT 59
                                                                                                                                                18 eLeuLysTrpLeuCysGluLysGlyPheAspvalileAlaTyrValAlaA 35
                                                                                                                                                                                                                           60 CCTCGTGTGGCTGAAGGAACAAGGCTATGACGTCATTGCCTATCTGGCCA 109
                                                                                                                                                                                                                                                                                                          35 snvalGlyGlnLysAspAspPheValAlaIleLysGluLysAlaLeuLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thermotogales; Thermotoga.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quality: 1226.50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       409 AA; 46054 MW; ECCDC8575E962482 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 139.50
139.00
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82.222
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157.27
153.63
151.21
146.01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        percent Identity: 59.012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0.2353
0.2763
0.2900
0.2995
0.3209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             301
629
956
1262
1296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | O62105 mus musculus (mouse).
| O9dwh3 rat cytomegalovirus (
| O9dg39 homo sapiens (human).
| O9ug49 homo sapiens (human)
| O9ug40 homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (mouse).
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us-09-775-693-1.rspt

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alignment_block:
US-09-775-693-1 x Q9RWJ4
                                                                                                                                                              alignment_scores:
                                              Align seg 1/1 to: Q9RWJ4 from: 1 to: 402
                                                                                                                Quality: 1034.00
Ratio: 3.272
Percent Similarity: 76.886
                                                                                                                                                                                                                                                                                  seq_documentation_block:
ID Q9RWJ4 PRELIMINARY;
7 AGCAAAGGCTCCGTGGTTCTGGCCTACAGTGGCGGGCCTGGACACCTCGTG 56
                                                                                                                                                                                                                  Pfam; PF00764; Arginosuc_synth; 1.
Probom; PF003544; Arginosuc_synth; 1.
PROSITE; PS00564; ARGININOSUCCIN_SYN_1; 1.
PROSITE; PS00565; ARGININOSUCCIN_SYN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seq_name: sp_bacteria:Q9RWJ4
                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                ATP-binding; Arginine biosynthesis; Complete proteome; Ligase;
                                                                                                                                                                                                                                                                                                                               InterPro, IPRO01518; Arginosuc_synth.
                                                                                                                                                                                                                                                                                -1- SIMILARITY: TO THE ARGININOSUCCINATE SYNTHASE FAMILY.
EMBL; AE001924; AAF10250.1; -.
TIGR; DR0674; -.
                                                                                                                                                                                                                                                                                                                        -!- SUBUNIT: HOMOTETRAMER (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                       White O., Elsen J.A., Heidelberg J.F., Hickey B.K., Peterson J.D., Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L., Weight K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M., Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D., Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C., Prace C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                    "Genome sequence of the radioresistant bacterium Deinococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                O9RWJ4;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
ARGININOSUCCINATE SYNTHASE (EC 6.3.4.5) (CITRULLINE--ASPARTATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Thermus/Deinococcus group; Deinococcales; Deinococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1210 CGTCTCCAGAGCAAG 1224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1160 ATGCCACCGGGTTCATCAACATCAATTCCCTCAGGCTGAAGGAATATCAT 1209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1110 CAATGAGGAGCTGGTGAGCATGAACGTGCAGGGTGATTATGAGGCAACTG 1159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            401 GlnLeuValLysLys 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          385 spSerLysGlyPheileAsnileHisAlaLeuArgLeuLys...ValHis 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           368 rAsnProGluLeuSerSerMetAspValGluGlyGlyPheAspAlaThrA 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          352 TyrLysClyAenValMetProValAlaArgTyrSerProTyrSerLeuTy 368
                                                                                                                                                                              402 AA; 44877 MW; 8694AD1424A99835 CRC64;
                                                                                                         Percent Identity: 50.122
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316 aSerLeuValTyrAsnGlyPheTrpPheSerProGluArgGluMetLeuG
                                                       954 TGAGCTGGTGTATACCGGTTTACGGCCTAGCCCTGAGTGTGAATTTGTCC 1003
                                                                                                                                                                            904 ATGGACCGGGAAGTGCGCAAAATCAAACAAGGCCTGGGCTTGAAATTTGC 953
                                                                                                                                                                                                                                                                                          854 CAGCAGGCACCATCCTTTACCATGCTCATTTAGACATCGAGGCCTTCACC 903
                                                                                                                                                                                                                                                                                                                                                        804 CGTGGAGAACCGCTTCATTGGAATGAAGTCCCGAGGTATCTACGAGACCC 853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   250 ThrLysLeuAsnGluLeuGlyArgAspAsnGlyValGlyArgLeuAspLe 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              754 ATGTACCTGAACGAAGTCGCGGGCAAGCATGGCGTGGGGCCGTATTGACAT 803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               704 TGACCAACGTCAAGGATGGCACCACCCACCAGACCTCCTTGGAGCTCTTC 753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 654 CACCCCTGACATTCTCGAGATCGAGTTCAAAAAAGGGGTCCCTGTGAAGG 703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                604 GCGCCTCCAGGTCTCTACACGAAGACCCAGGACCCAGGCCAAAGCCCCCAA 653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         171 nIleThrLysAspLysArgGlyGluAlaProPheSerValAspAlaAsnL 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   510 CATCCCGGTCACTCCCAAGAAC.....CCGTGGAGCATGGATGAGAACC 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       155 PheLysSerArgGluAlaLeuLeuAspPheAlaGluLysHisGlnIleGl 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  460 TTCAAGGGCCGCAATGACCTGATGGAGTACGCAAAGCAACACGGGATTCC 509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            142 roAspIleThrValIleAlaProTrpArgGluTrpAsp......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   410 CCCAGATAAAGGTCATTGCTCCCTGGAGGATGCCTGAATTCTACAACCGG 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           125 yLysGlyAsnAspGlnValArgPheGluLeuGlyTyrTyrGlyLeuGluP 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             109 GluIleAlaArgLysMetGlyAlaAspAlaValSerHisGlyAlaThrGl 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     360 AAAGGGGAACGATCAGGTCCGGTTTGAGCTCAGCTGCTACTCACTGGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    310 GAAATCGCCCAGCGGGAGGGGGCCAAGTATGTGTCCCACGGCGCCCACAGG 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      260 ACCTCCTGGGCACCTCTTGCCAGGCCCTGCATCGCCCGCAAACAAGTG 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    210 GGAGTTCATCTGGCCGGCCATCCAGTCCAGCGCACTGTATGAGGACCGCT 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   166 GCCAAA.....AAGGTGTTCATTGAGGATGTCAGCAGGGAGTTTGTGGA 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92 yrLeuLeuGlyThrSerIleAlaArgProLeuIleAlaLysLysGlnIle 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             75 gAspTyrValPheProMetPheArgAlaAsnThrValTyrGluGlyGlnT 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59 ValLysProGluAsnIlePheIleGluAspValArgGluGluPheValAr 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42
                                                                                                                 LeuAspArgGlyAlaMetHisLeuLysAspGluLeuMetProLysTyrAl 316
                                                                                                                                                                                                                                      {\tt roGlyGlyThrIleLeuLeuAlaAlaHisArgGlyIleGluSerIleThr}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        le.....AspGlyValAla...MetSerProAlaThrLeuLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pAlaProThrIleIleThrIleAspPheGluLysGlyAspProValAlaI 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        {\tt AlaProGluPheValHisMetArgThrIleAlaProGluAspAlaProAs}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          euLeuHisSerSerSerGluGlyLysValLeuGluAspProAlaValGlu
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Seq_documentation_block:
ID Q9HY84
AC Q9HY84
DT 01-MAR-2001 (TrEMBLre DF 2001 (TrEMBLre DF 2001 (TrEMBLre DF 2001 (TrEMBLre DF 2001 (TrEMBLRE SYN 2001 (TREMBLE SYN 2001 (TREMBLRE SYN 2001 (TREMBLRE SYN 2001 (TREMBLRE SYN 2001 (T
alignment_scores:
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ProDom; PD003544; Arginosuc_synth; 1.
PROSITE; PS00564; ARGININOSUCCIN_SYN_1; 1.
PROSITE; PS00565; ARGININOSUCCIN_SYN_2; 1.
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Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,
Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
"Complete genome sequence of Pseudomonas aeruginosa PAO1, an
opportunistic pathogen.";
Nature 406.959-964(2000).
-i- CATALYTIC ACTIVITY: ATP + L-CITRULLINE + L-ASPARTATE = AMP +
PYBOPHOSPHAYE + L-ARGINIOSUCCINATE.
                                                                                                                                                                        ATP-binding; Arginine biosynthesis; Complete proteome; Ligase;
                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001518; Arginosuc_synth.
                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SIMILARITY: TO THE ARGININOSUCCINATE SYNTHASE FAMILY EMBL; AE004773; AAG06913.1; -
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-1- SUBUNIT: HOMOTETRAMER (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- PATHWAY: UREA CYCLE, PENULTIMATE STEP OF THE ARGININE BIOSYNTHETIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1148 ATGAGCCAACTGATGCCACCGGGTTCATCAACATCAATTCCCTCAGGCTG 1197
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
ARGININOSUCCINATE SYNTHASE (EC 6.3.4.5) (CITRULLINE--ASPARTATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1198 AAG 1200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     350 LysLeuTyrLysGlyAsnValThrValIleGlyArgGluSerProTyrSe 366
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                                                                                                     405 AA; 45297 MW; 1C3DB39EB18689E5 CRC64;
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alignment_block:

Percent Similarity:

927.50 3.011 76.238

Percent Identity: 47.030

Length:

Quality: Ratio:

US-09-775-693-1 x Q9HY84

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Align seg 1/1 to: Q9HY84 from: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hrPheThrAlaAspLeuGlyGlnGlyGluGluValGluProAlaArgAla 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCTATCTGGCCAACATTGGCCAGAAGGAAGACTTCGAGGAAGCCAGGAAG 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          yrAlaLeuLysProGlyValLysValIleAlaProTrpArgGluTrpAsp 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGGATGAGAACCTCATGCACATCAGCTACGAGGCTGGAATCCTGGAGAAC
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                                                                                                                                                                                                                                                                                                                                                                                                           ThrTrpThrGluHisGluGluAspMetTrpLysTrpThrAlaSerProGl 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCCAAGAACCAAGCGCCTCCAGGTCTCTACACGAAGACCCAGGACCCAGC
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                                                                                                                                                                               TTGGAGCTCTTCATGTACCTGAACGAAGTCGCGGGCAAGCATGGCGTGGG 791
                                                                                                                                                                                                                          spIleValAlaIle......AspGly...LysAspMetThrPro
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    891
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seq_documentation_block:
ID Q9PHK7 PRELIMINARY;
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Parkhill J., Wren B.W., Mungall K., Ketley J.M., Churcher C.,
Basham D., Chillingworth T., Davies R.M., Feltwell T., Holroyd S.
Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,
Quail M.A., Rajandream M.A., Rutherford K.M., Van Vliet A.H.M.,
Whitehead S., Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last Sequence update)
01-UN-2001 (TrEMBLrel. 17, Last annotation update)
ARGININOSUCCINATE SYNTHASE (EC 6.3.4.5) (CITRULLINE--ASPARTATE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. STRAIN=NCTC 11168; MEDLINE=20150912; I
                               Pfam; PF00764; Arginosuc_synth; 1.
ProDom; PD003544; Arginosuc_synth; 1.
PROSITE; PS00564; ARGININOSUCCIN_SYN_1; 1.
PROSITE; PS00565; ARGININOSUCCIN_SYN_2; 1.
ATP-binding; Arginine biosynthesis; Complete proteome; Ligase;
                                                                                                                                                                                                                                                                              reveals hypervariable sequences.";
Nature 403:665-668(2000).
-i- CATALYTIC ACTIVITY: ATP + L-CITRULLINE + L-ASPARTATE = AMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group;
                                                                                                                                   -i- SIMILARITY: TO THE ARGININOSUCCINATE SYNTHASE FAMILY EMBL; AL139075; CAB75297.1; -. InterPro; IPR001518; Arginosuc_synth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Campylobacter jejuni.
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                                                                                                                                                                                                                                                                                                                                           "The genome sequence of the food-borne pathogen Campylobacter jejuni
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Campylobacter
  SEQUENCE
                       Urea cycle.
                                                                                                                                                                                                  -!- SUBUNIT: HOMOTETRAMER (BY SIMILARITY)
                                                                                                                                                                                                                                      -!- PATHWAY: UREA CYCLE, PENULTIMATE
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                                                                                                                                                                                                                     PATHWAY.
                                                                                                                                                                                                                                                             PYROPHOSPHATE + L-ARGININOSUCCINATE
  406 AA; 45578 MW; 8A1E137AF30EC77F CRC64;
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                                                                                                                                                                                                                                                 THE ARGININE BIOSYNTHETIC
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alignment_scores:
    Quality:
    Ratio:
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US-09-775-693-1 x Q9PHK7 ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1 to: Q9PHK7 from: 1 to: 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
                                                             237 snGlyGluLys.....LeuSerProAlaGlyLeuLeuThr 248
757 TACCTGAACGAAGTCGCGGGCAAGCATGGCGTGGGCCCTATTGACATCGT 806
                                                                                                                                            220 uSerGluIleIleGluLeuAspPheGlnLysGlyAspLeuValAlaIleA 237
                                                                                                                                                                                     657 CCCTGACATTCTCGAGATCGAGTTCAAAAAAGGGGGTCCCTGTGAAGGTGA 706
                                                                                                                                                                                                                               204 GluGluAspMetTrpArgTrpSerLysSerProLysAspAlaProAsnGl 220
                                                                                                                                                                                                                                                                      607 CCTCCAGGTCTCTACACGAAGACCCAGGACCCAAGCCCAAAGCCCCCAACAC 656
                                                                                                                                                                                                                                                                                                              557 TGCACATCAGCTACGAGGCTGGAATCCTGGAGAACCCCAAGAACCAAGCG 606
                                                                                                                                                                                                                                                                                                                                                                                               158 GluLys.....LeuLeuAlaTyrAlaGlnLysHisGlyIleAs 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        460 TTCAAGGGCCGCAATGACCTGATGGAGTACGCAAAGCAACACGGGATTCC 509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               141 roAspLeuLysIleIleAlaProTrpArgGluTrpAspLeuAsnSerArg 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     360 AAAGGGGAACGATCAGGTCCGGTTTGAGCTCAGCTGCTACTCACTGGCCC 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           410 CCCAGATAAAGGTCATTGCTCCCTGGAGGATGCCTGAATTCTACAACCGG 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  124 yLysGlyAsnAspGlnValArgPheGluLeuGlyTyrLeuAlaPheSerP 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       108 GinIleAlaLeuGinThrGlyAlaAspAlaValSerHisGlyAlaThrGl 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            310 GAAATCGCCCAGCGGAGGGGGCCAAGTATGTGTCCCACGGCGCCACAGG 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           260 ACCTCCTGGGCACCTCTCTTGCCAGGCCCTGCATCGCCCGCAAACAAGTG 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             210 GGAGTTCATCTGGCCGGCCATCCAGTCCAGCGCACTGTATGAGGACCGCT 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  166 GCCAAAAAG......GTGTTCATTGAGGATGTCAGCAGGGAGTTTGTGGA 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           116 GCCAGAAGGAAGACTTCGAGGAAGCCAGGAAGAAGGCACTGAAGCTTGGG 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   74 SASPTYTVAlPheProMetPheArgAlaAsnAlaIleTyrGluGlyGluT 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58 IleLysGluGluAsnIlePheIleLysAspLeuArgAspGluPheValLy 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24 pLeuGlnAspGluTyrAsnCysGluValValThrPheThrAlaAspIleG 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               69 GCTGAAG...GAACAAGGCTATGACGTCATTGCCTATCTGGCCAACATTG 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCAACGTCAAGGATGGCACCACCCACCAGACCTCCTTGGAGCTCTTCATG 756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       892.00
3.014
74.559
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Percent Identity: 47.355
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igase;	<pre>ATP-Binding; Arginine biosynthesis; Complete proteome; L Urea cycle.</pre>	
	PROSITE; PS00565; ARGININOSUCCIN_SYN_2; 1.	
	DR PROSITE: PS00564: Arginosuc_synth; 1.	
	DR Pfam; PF00764; Arginosuc_synth; 1.	
٠	EMBL; AP001518; BAB06906.1;	
	CC -:- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).	
E 0103	PATHWAY.	
F DIOCVIMUENT	-1- PATHWAY: UREA CYCLE, PENULTIMATE STED OF THE ADCININ	
= AMP +	CC -!- CATALYTIC ACTIVITY: ATP + L-CITRULLINE + L-ASPARTATE	
subtil	Nucleic Acids Res. 28:4317-4331(2000).	
Bacillus	"Complete genome sequence of the alkaliphilic bacterium	
-	Horikoshi K.;	
Masui N.,	Pudi F. Hirama C. Nakamira v. Cananana V. Sasaki R.,	
	MEDLINE=20512582; PubMed=1105	
	SEQUENCE FROM N	
	Bacillus/Staphylococcus g	
	Bacillus halodurans. Bacteria: Firmicutes: Bacillus/Clostridium group	
	ARGG OR	
PARTATE	ARGININOSUCCINATE SYNTHASE (EC 6.3.4.5) (CITRULL LIGASE).	
	01-JUN-2001 (TrembLrel. 17, Last annotation update	
	01-OCT-2000 (TrEMBLrel 15, Created)	
	Q9K820;	
	q_documentation_block:	
	seq_name: sp_bacteria:Q9K820	
	1154 CAACTGATGCCACCGGGTTCATCAACATCAATTTCCCTCAGG 1194 ::: :::: ::: :::	
382	365 rLeuPheAsnAlaAlaTyrCysThrPheGluGluAspGluValTyrAsnG	
i	04 TCTCTACAATGAGGAGCTGGTGAGCATGAACGTGCAGGGTGATTATGAGC	
365	349 LeuTyrLysGlyAsnValMetValIleGlyArgGluSerAlaAsnAspSe	
348	332 laLeuIleAspGluSerGlnIleHisAlaAsnGlyArgValLysLeuGlu	
1056	CAAGTCCCAGGAGCGAGTGGAAGGGAAAGTGCAGGTGTCC	
332	315 rLeuileTyrAsnGlyTyrTrpPheSerProGluArgMetMetLeuGlnA	
1006	GTATACCGGTTTACGGCCTAGCCCTGAGTGTGAATTTGTCC	
956 315	907 GACCGGGAAGTGCGCAAAATCAAACGAGGCCTGGGCTTGAAATTTGCTGA	
298	oz iyeiyTHTiTeLeuLeuLysAlaHiSArgAlaLeuGluSerIleThr	
906	57 CAGGCACCATCCTTTACCATGCTCATTTAGA	
	265 lGluAsnArgTyrValGlyMetLysSerArgGLyCysTyrGluThrProG	
856	GAGAACCGCTTCATTGGAATGAAGTCCCGAGGTATCTACGAGACCCC	
265	z + 7 HysheumshoruheumrycyshyshisGiylleGiyArgLeuAspIleVa	

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us-09-775-693-1.rspt

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alignment_scores:
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Ratio: 2.912
Percent Similarity: 72.439
230 ..AsnGlyLysSerTyrProValHis.....GluLeuIleLeu 241
                                              707 CCAACGTCAAGGATGGCACCACCACCAGACCTCCTTGGAGCTCTTCATG 756
                                                                                                                                             657 CCCTGACATTCTCGAGATCGAGTTCAAAAAAAGGGGTCCCTGTGAAGGTGA 706
                                                                                                                                                                                              197 ProGluGlyAlaTyrGluLeuThrValAlaIleGluAspAlaProAspGl 213
                                                                                            213 nProGluIleValGluIleGlyPheGluLySGlyIleProValThrLeu. 229
                                                                                                                                                                                                                                                                                          180 rpGlyArgSerAsnGluCysGlyIleLeuGluAspProTrpAlaThrPro 196
                                                                                                                                                                                                                                                                                                                                         557 TGCACATCAGCTACGAGGCTGGAATCCTGGAGAACCCCAAGAACCAAGCG 606
                                                                                                                                                                                                                                                                                                                                                                                       163 eProIleProIleAspLeuAspAsnProTyrSerValAspGlnAsnLeuT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                     507 TCCCATCCCGGTCACTCCCAAGAACCCGTGGAGCATGGATGAGAACCTCA 556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      150 .....SerArgAspGluGluIleGluTyrAlaLysLysAsnAsnIl 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    457 CGGTTCAAGGGCCGCAATGACCTGATGGAGTACGCAAAGCAACACGGGAT 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   135 snProAsnLeuGluValLeuAlaProValArgGluTrpAlaTrp..... 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 407 CCCCCCAGATAAAGGTCATTGCTCCCTGGAGGATGCCTGAATTCTACAAC 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              357 AGGAAAGGGGAACGATCAGGTCCGGTTTGAGCTCAGCTGCTACTCACTGG 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -09-775-693-1 ж Q9К820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              102 ValGlurleAlaGluGlnThrGlyAlaGlnAlaValAlaHisGlyCysTh 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               307 GTGGAAATCGCCCAGCGGGAGGGGGCCAAGTATGTGTCCCACGGCGCCAC 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            257 GCTACCTCCTGGGCACCTCTCTTGCCAGGCCCTGCATCGCCCGCAAACAA 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        207 GGAGGAGTTCATCTGGCCGGCCATCCAGTCCAGCGCACTGTATGAGGACC 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              85 ysTyrProLeuValSerAlaLeuSerArgProLeuIleSerLysLysLeu 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  107 CCAACATTGGCCAGAAGGAAGACTTCGAGGAAGCCAGGAAGAAGGCACTG 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       52 LysValGlyAlaIleGluSerTyrThrIleAspAlaLysLysGluPheAl 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      35 euAspValGlyGluGlyLysAspLeuGluPheValLysGluLysAlaLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18 lAlaIleLysTrpLeuSerAspLysGlyTyrAspValIleAlaValGlyL 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57 CATCCTCGTGTGGCTGAAGGAACAAGGCTATGACGTCATTGCCTATCTGG 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 AGCAAAGGCTCCGTGGTTCTGGCCTACAGTGGCGGCCTGGACACCTCGTG 56
                                                                                                                                                                                                                                            CCTCCAGGTCTCTACACGAAGACCCAGGACCCAGCCAAAGCCCCCAACAC 656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rGlyLysGlyAsnAspGlnValArgPheGluValSerIleGlnAlaLeuA 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          aGluGluPheValLeuProAlaLeuGlnAlaHisAlaLeuTyrGluGlnL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAGCTTGGGGCCAAAAAGGTGTTCATTGAGGATGTCAGCAGGGAGTTTGT 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 409 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51
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seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_name: sp_bacteria:09K4Z3
            PATHWAY.

PATHWA
InterPro; IPR001518; Arginosuc_synth
                                                                                                                                                                                                                                 Xu Y. Liang Z., Legrain C., Ruger H.J., Glansdorff N.; "Evolution of Arginine biosynthesis in the bacterial domain: Novel gene-enzyme relationships from psychrophilic moritella strains (vibrionaceae) and evolutionary significance of n-alpha-acetyl ornithinase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1157 CTGATGCCACCGGGTTCATCAACATCAATTCCCTCAGGCTGAAGGAATAT 1206
                                                                                                                                                                                -!- PATHWAY: UREA CYCLE, PENULTIMATE STEP OF THE ARGININE BIOSYNTHETIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1107 CTACAATGAGGAGCTGGTGAGCATGAACGTGCAGGGTGATTATGAGCCAA 1156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1207 CATCGTCTCCAGAGCAAGGTCACTGCCAAA 1236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=20158877; PubMed=10692366;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=2674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; gamma subdivision; Alteromonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ARGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
ARGININOSUCCINATE SYNTHASE (EC 6.3.4.5) (CITRULLINE--ASPARTATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1007 ACTGCATCGCCAAGTCCCAGGAGCGAGTGGAAGGGAAAGTGCAGGTGTCC 1056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 392 SerMetValAsnLysGluMetLysGluLys 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Moritella sp. 2674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LIGASE).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             375 snAlaAlaValGlyPheIleSerLeuTrpGlyLeuProThrLysValTyr 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=111291;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                342 LeuPheLysGlyHisAlaIleValGluGlyArgLysSerGluTyrSerLe 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            325 laPheLeuLysGluThrGlnSerThrValThrGlyValValArgValLys 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    308 uLeuIleTyrGluGlyLeuTrpPheSerProLeuGlnProAlaLeuSerA 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              957 GCTGGTGTATACCGGTTTACGGCCTAGCCCTGAGTGTGAATTTGTCCGCC 1006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    292 ThrLysGluValAlaHisPheLysProValValGluLysLysIleAlaGl 308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          857 CAGGCACCATCCTTTACCATGCTCATTTAGACATCGAGGCCTTCACCATG 906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        757 TACCTGAACGAAGTCGCGGGCAAGCATGGCGTGGGCCGTATTGACATCGT 806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    258 lGluAsnArgLeuValGlyIleLysSerArgGluValTyrGluCysProG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              807 GGAGAACCGCTTCATTGGAATGAAGTCCCGAGGTATCTACGAGACCCCAG 856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        404 AA
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SQ KW
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US-09-775-693-1 x Q9K4Z3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Align seg 1/1 to: Q9K4Z3 from: 1 to: 404
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proStTE; ps00564; ARGININOSUCCIN_SYN_2; 1.
prOSTTE; ps00565; ARGININOSUCCIN_SYN_2; 1.
proStTE; 1.
proDom; PD003544; Arginosuc_synth; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 157 AAGCTTGGGGCCAAAAAGGTGTTCATTGAGGATGTCAGCAGGGAGTTTGT 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 110 ACATTGGCCAG...AAGGAAGACTTCGAGGAAGCCAGGAAGAAGGCACTG 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    257 GCTACCTCCTGGGCACCTCTCTTGCCAGGCCCTGCATCGCCCGCAAACAA 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   207 GGAGGAGTTCATCTGGCCGGCCATCCAGTCCAGCGCACTGTATGAGGACC 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19 GTGGTTCTGGCCTACAGTGGCGGCCTGGACACCTCGTGCATCCTCGTGTG 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  170 pIleProThrAlaAlaSerAlaThrLysIleTyrSerArgAspAlaAsnA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    504 GATTCCCATCCCGGTCACTCCCAAGAACCCGTGGAGCATGGATGAGAACC 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             454 AACCGGTTCAAGGGCCGCAATGACCTGATGGAGTACGCAAAGCAACACGG 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            404
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 75 lGluAsnTyrIleTyrProThrLeuLysThrGlyAlaValTyrGluGlyT 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59 AlaSerGlyAlaSerGluCysTyrValValAspLeuLysAspGluLeuVa 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26 pLeuGlnGlu...AsnTyrAspAsnCysGluIleValAlaPheValAlaA 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          69 GCTGAAGGAACAAGGCTATGAC......GTCATTGCCTATCTGGCCA 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10 ValValValAlaTyrSerGlyGlyLeuAspThrSerValIleLeuProTr 26
                                                                                                                                                                                                                                                                                                                                                                                   187 laTrpHisIleSerHisGluGlyGlyGluLeuGluAspProTrpAsnGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                554 TCATGCACATCAGCTACGAGGCTGGAATCCTGGAGAACCCAAGAACCAA 603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           156 .....LeuThrSerArgGluSerLeuLeuGluTyrLeuAlaGluArgAs 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       654 CACCCCTGACATTCTCGAGATCGAGTTCAAAAAAGGGGGTCCCTGTGAAGG 703
                                                                                                                                                                                    204 ProSerLysGlnValTrpThrMetThrValAspProIleAspAlaProAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              spValGlyGinGlyAlaGluGluLeuGluGlyIleGluAlaLysAlaLeu 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGGAAAGGGGAACGATCAGGTCCGGTTTGAGCTCAGCTGCTAC...TCAC 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ValGluIleAlaArgLysValGlyAlaAspAlaLeuCysHisGlyCysTh 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTGGAAATCGCCCAGCGGGAGGGGGCCAAGTATGTGTCCCACGGCGCCCAC 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               euAlaProGluLeuThrValIleAlaProTrpArgIleTrpAsp..... 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGGCCCCCAGATAAAGGTCATTGCTCCCTGGAGGATGCCTGAATTCTAC 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rGlyLysGlyAsnAspGlnIleArgPheGlu...SerCysPheAlaAlaL
                                                                                                                                                                                                                                                                                           GCGCCTCCAGGTCTCTACACGAAGACCCAGGACCCAGCCAAAGCCCCCAA 653
nGluProGluPheLeuThrIleSerValValLysGly...GluIleThrA 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Quality:
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seq_name: sp_plant:Q9SZX3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1004 GCCACTGCATCGCCAAGTCCCAGGAGCGAGTGGAAGGGAAAGTGCAGGTG 1053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1154 CAACTGATGCCACCGGGTTCATCAACATCAATTCCCTC.....AGGCTG 1197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1104 TCTCTACAATGAGGAGCTGGTGAGCATGAACGTGCAGGGTGATTATGAGC 1153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           854 CAGCAGGCACCATCCTTTACCATGCTCATTTAGACATCGAGGCCTTCACC 903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               804 CGTGGAGAACCGCTTCATTGGAATGAAGTCCCGAGGTATCTACGAGACCC 853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                236 laValAsnGlyGluAlaMetSerProTyrAsnThr.....Leu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          704 TGACCAACGTCAAGGATGGCACCACCCACCAGACCTCCTTGGAGCTCTTC 753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1198 AAG 1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 315 rHisLeuValTyrAspGlyArgTrpPheThrProLeuCysAlaSerLeuL 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             954 TGAGCTGGTGTATACCGGTTTACGGCCTAGCCCTGAGTGTGAATTTGTCC 1003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       299 LeuAspLysThrThrArgLysTrpLysGlnThrValAlaAlaGluPheSe 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      365 rLeuTyrSerGluGluPheAlaThrPheGlyAspAspAsnValTyrAspG 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          349 LysMetTyrLysGlySerValGlnAlaIleGlnLysLysSerProAsnSe 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               332 euAlaAlaGlyThrLeuAlaGluGluMetAsnGlyGluValIleVal 348
                                                                                                                                                                                                                                                                                                                                                                                              01-MAY 2000 (TremBLrel. 13, Created)
01-MAY 2000 (TremBLrel. 13, Last sequence update)
01-JUN-2001 (TremBLrel. 17, Last annotation update)
ARGININOSUCCINATE SYNTHASE-LIKE PROTEIN (EC 6.3.4.5).
F617.40 OR AT4G24830.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               382 lnSerHisAlaGluGlyPheIleArgLeuTyrSerLeuSerSerArgIle 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             399 Lys 399
                                                                                                                         Bevan M., Terryn N., Ardiles W., Buysshaert C., Dasseville R., De Clerck R., De Keyser A., Neyt P., Rouze P., Van Den Daele H., Villaroel R., Gielen J., Van Montagu M., Bancroft I., Hoheisel J., Mewes H.W., Mayer K.F.X., Schueller C.; Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9SZX3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9SZX3
                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana (Mouse-ear cress).
                                          EU Arabidopsis sequencing project; submitted (APR-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                       NCBI_TaxID=3702;
SEQUENCE FROM N.A.
                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       eValGluAsnArgLeuValGlyMetLysSerArgGlyCysTyrGluThrP 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATGGACCGGGAAGTGCGCAAAATCAAACAAGGCCTGGGCTTGAAATTTGC 953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 roGlyGlyThrValMetValGluAlaLeuArgGlyIleGluGluLeuVal 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             498 AA.
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SQ SQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Quality: 815.00
Ratio: 2.890
Percent Similarity: 71.212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Align seg 1/1 to: Q9SZX3 from: 1 to: 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-775-693-1 x Q9SZX3
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proDom; pD003544; Arginosuc_synth; 1.
prOSITE; pS00564; ARGININOSUCCIN_SYN_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE 498 AA; 54880 MW; BCD9A856E5F50D5C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         128 ValValLeuAlaTyrSerGlyGlyLeuAspThrSerValIleValProTr 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        163 GGGGCCAAAAAGGTGTTCATTGAGGATGTCAGCAGGGAGTTTGTGGAGGA 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               161 lyGlnGlyIleLysGluLeuGluGlyLeuGluGlnLysAlaLysAlaSer 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   116 GCCAGAAG...GAAGACTTCGAGGAAGCCAGGAAGAAGGCACTGAAGCTT 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        144 pLeuLysGluAsnTyrGlyCysGluValValCysPheThrAlaAspValG 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          313
                                                                                                                                                                                                                                                                                                                                249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            363 GGGGAACGATCAGGTCCGGTTTGAGCTCAGCTGCTACTCACTGGCCCCCC 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      223
                                                                                                                                                                                                                                                                                                                                                                                    463 AAGGGCCGCAATGACCTGATGGAGTACGCAAAGCAACACGGGATTCCCAT 512
                                                    613 GGTCTCTACACGAAGACCCCAGGACCCAGCCCAAAGCCCCCCAACACCCCCTGA 662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               69 GCTGAAGGAACAA...GGCTATGACGTCATTGCCTATCTGGCCAACATTG 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19 GTGGTTCTGGCCTACAGTGGCGGCCTGGACACCTCGTGCATCCTCGTGTG 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pPheIlePheProCysLeuArgAlaGlyAlaIleTyrGluArgLysTyrL 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTTCATCTGGCCGGCCATCCAGTCCAGCGCACTGTATGAGGACCGCTACC 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GlyAlaSerGlnLeuValValLysAspLeuThrGluGluPheValLysAs 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCCTGGGCACCTCTTGCCAGGCCCTGCATCGCCCGCAAACAAGTGGAA 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGATAAAGGTCATTGCTCCCTGGAGGATGCCTGAATTCTACAACCGGTTC 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               euLeuGlyThrSerMetAlaArgProValIleAlaLys..... 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATCGCCCAGCGGGAGGGGCCAAGTATGTGTCCCACGGCGCCACAGGAAA 362
AspMetTyrMetMetSerValAspProGluAspAlaProAspGlnProGl 315
                                                                                                     euSerHisGluGlyAspLeuLeuGluAspProAlaAsnGluProLysLys 298
                                                                                                                                                             TCAGCTACGAGGCTGGAATCCTGGAGAACCCCAAGAACCAAGCGCCTCCA 612
                                                                                                                                                                                                                    lProvalThrLysLysSerIleTyrSerArgAspArgAsnLeuTrpHisL 282
                                                                                                                                                                                                                                                                           CCCGGTCACTCCCAAGAACCCGTGGAGCATGGATGAGAACCTCATGCACA 562
                                                                                                                                                                                                                                                                                                                                GlnGlyArgGluAspAlaIleGluTyrAlaLysLysHisAsnValProVa 265
                                                                                                                                                                                                                                                                                                                                                                                                                                           luLeuLysValValAlaProTrpArgGluTrpGlu......Ile 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Identity: 42.172
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seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1163 CCACCGGGTTCATCAACATCAATTCCCTCAGGCTGAAG 1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1113 TGAGGAGCTGGTGAGCATGAACGTGCAGGGTGATTATGAGCCAACTGATG 1162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1063 AAGGGCCAGGTGTACATCCTCGGCCGGGAGTCCCCACTGTCTCTCTACAA 1112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               315 uTyrIleGluIleGlyIleGluSerGlyLeuProValAlaLeuAsnGly. 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    663 CATTCTCGAGATCGAGTTCAAAAAAGGGGTCCCTGTGAAGGTGACCAACG 712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 344 AsnThrIleGlyGlyLysHisGlyIleGlyArgIleAspMetValGluAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    713 TCAAGGATGGCACCACCACCAGACCTCCTTGGAGCTCTTCATGTACCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               410 lTyrAlaGlyArgTrpPheAspProLeuArgGluSerMetAspAlaPheM 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               394 GluSerIleGlnValLysAspThrLeuAlaLeuLysTyrAlaGluMetVa 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      863 CCATCCTTTACCATGCTCATTTAGACATCGAGGCCTTCACCATGGACCGG 912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               813 CCGCTTCATTGGAATGAAGTCCCGAGGTATCTACGAGACCCCAGCAGGCA 862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     763 AACGAAGTCGCGGGCAAGCATGGCGTGGGCCGTATTGACATCGTGGAGAA 812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 477 laAlaGlyPheIleArgLeuTyrGlyLeuProMetLys 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 460 gGlnAspIleSerSerPheGluGlySerGluIleTyrAsnGlnAlaAspA 477
                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UUN-2001 (TrEMBLrel. 17, Last annotation update)
ARGININOSUCCINATE SYNTHASE (EC 6.3.4.5) (CITRULLINE--ASPARTATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9K4Y8
                                                                           MEDLINE-20158877; PubMed=10692366; Xu Y., Liang Z., Legrain C., Ruger H.J., Glansdorff N.; Xu Y., Liang Z., Legrain C., Ruger the bacterial domain: Novel gene-enzyme relationships from psychrophilic moritella strains (vibrionaceae) and evolutionary significance of n-alpha-acetyl ornithinase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9K4Y8;
                     J. Bacteriol. 182:1609-1615(2000).

-i- CATALYTIC ACTIVITY: ATP + L-CITRULLINE + L-ASPARTATE = AMP + PYROPHOSPHATE + L-ARGININOSUCCINATE.
                                                                                                                                                                                                                                                                 NCBI_TaxID=111292;
                                                                                                                                                                                                                                                                                           Moritella.
                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; gamma subdivision; Alteromonadaceae;
                                                                                                                                                                                                                                                                                                                                  Moritella sp. 2693
                                                                                                                                                                                                                                                                                                                                                     ARGG
                                                                                                                                                                                                                                                                                                                                                                         LIGASE).
                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAAGTGCGCAAAATCAAACAAGGCCTGGGCTTGAAATTTGCTGAGCTGGT 962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTATACCGGTTTACGGCCTAGCCCTGAGTGTGAATTTGTCCGCCACTGCA 1012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hrIleLeuPheAlaAlaValGlnGluLeuGluSerLeuThrLeuAspArg
PATHWAY: UREA CYCLE, PENULTIMATE STEP OF THE ARGININE BIOSYNTHETIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      404 AA
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alignment_scores:
Quality:
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C -!- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).

C -!- SIMILARITY: TO THE ARGININOSUCCINATE SYNTHASE FAMILY.

R EMBL; AJ252021; CAB95033.1; -.

R InterPro; IPR001518; Arginosuc_synth.

Pfam; pF00764; Arginosuc_synth; 1.

DR ProDom; PD003544; Arginosuc_synth; 1.

DR PROSTITE; PS00564; ARGININOSUCCIN_SYN_1; 1.

DR PROSTITE; PS00564; ARGININOSUCCIN_SYN_2; 1.

DR PROSTITE; PS00565; ARGININOSUCCIN_SYN_2; 1.

RW ATP-binding; Arginine biosynthesis; Ligase; Urea cycle.

SQ SEQUENCE 404 AA; 44432 MW; 9E1C4D037AF5923F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1 to: Q9K4Y8 from: 1 to: 404
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quality: 776.00
Ratio: 2.713
Percent Similarity: 70.968
          601 CAAGCGCCTCCAGGTCTCTACACGAAGACCCAGGACCCAGGCCAAAGCCCC 650
                                              551 ACCTCATGCACATCAGCTACGAGGCTGGAATCCTGGAGAACCCCAAGAAC 600
                                                                                                                         168 gAspIleProThrAlaAlaSerGlyThrLysIleTyrSerArgAspAlaA 185
                                                                                                                                                                501 CGGGATTCCCATCCCGGTCACTCCCAAGAACCCCGTGGAGCATGGATGAGA 550
                                                                                                                                                                                                       155 .....LeuThrSerArgGluSerLeuLeuGluTyrLeuAlaGluAr 168
                                                                                                                                                                                                                                                                                                                                                         451 TACAACCGGTTCAAGGGCCGCAATGACCTGATGGAGTACGCAAAGCAACA 500
                                                                                                                                                                                                                                                                                401 CACTGGCCCCCAGATAAAGGTCATTGCTCCCTGGAGGATGCCTGAATTC 450
                                                                                                                                                                                                                                                                                                                                                                                                                                  304 CAAGTGGAAATCGCCCAGCGGGAGGGGGCCCAAGTATGTGTCCCACGGCGC 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          254 ACCGCTACCTCGGGCACCTCTCTTGCCAGGCCCTGCATCGCCGCGAAA 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               204 TGTGGAGGAGTTCATCTGGCCGGCCATCCAGTCCAGCGCACTGTATGAGG 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          154 CTGAAGCTTGGGGCCAAAAAGGTGTTCATTGAGGATGTCAGCAGGGAGTT 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   107 CCAACATTGGCCAG...AAGGAAGACTTCGAGGAAGCCCAGGAAGAAGGCA 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90 lyThrTyrLeuLeuGlyThrSerMetAlaArgGlnSerIleAlaLysAla 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          57 LeuAlaSerGlyAlaSerGluCysTyrValValAspLeuLysAspGluLe 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40 laAspValGlyGlnGlyAlaGluGluLeuGluGlyIleGluAlaLysAla 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                69 GCTGAAGGAACAAGGCTATGAC......GTCATTGCCTATCTGG 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24 pLeuGlnGlu...AsnTyrAspAsnCysGluIleValAlaLeuPheValA 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19 GTGGTTCTGGCCTACAGTGGCGGCCTGGACACCTCGTGCATCCTCGTGTG 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length: 403
Gaps: 10
Percent Identity: 43.672
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RP RA RA RA	ROCCO	DT DT DE GN		397	- -											
SEQUE SEQUE Kurodi Cui L Cui L Matsu Matsu Matsu Hiraka	Staph Bacte Bacil NCBI_	01-JU 01-JU 01-JU 01-JU ARGIN ARGG	10cumen 099VC7		.150 380 192	363	1051 (3 47)	330	951 313	901 297	851 280	801 263	751 247	701 232	651 218	202
SEQUENCE FROM N.A. KUTOda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Cui L., Oguchi A., Aoki K.I., Nagai Y., Lian J., Tit. Matsumaru H., Waruyama A., Murakamai H., Hosoyama A., Takahashi N.K., Sawano T., Inoue R.I., Kalto C., Sel	hylococcus aureus subsp. aureus eria; Firmicutes; Bacillus/Clos llus/Staphylococcus group; Stap _TaxID=158879;	JUN-2001 (TrEMBLrel. 17, Created JUN-2001 (TrEMBLrel. 17, Last se JUN-2001 (TrEMBLrel. 17, Last an INIOSUCCINATE SYNTHASE.	C7; PRELIMINARY; PRT;	ArgileLys 399	GAGCCAACTGATGCCACCGGGTTCATCAACATCAATTCCCTC :::	GTCTCTCTACAATGAGGAGCTGGTGAGCATGAACGTGCAGGGTGATTAT ::: ::::::::::::::::	GTGTCCGTCCTCAAGGGCCAGGTGTACATC	e :: 17			L CCCCAGCAGGCACCATCCTTTACCATGCTCATTTAGACATCGAGGCCTTC ::: :::::	1 CATEGTGGAGAACCGCTTCATTGGAATGAAGTCCCGAGGTATCTACGAGA 	TTCATGTACCTGAACGAAC ::: TyrThrTyrLeuAsnGluI	1 AGGTGACCAACGTCAAGGATGGCACCACC ::::: ::: 2 lulleThrAlaValAsnGlyGluGluMetTyr	CAACACCCCTGACATTCTCGAGATCGAG	2 GlnProSerLysGlnValTrpThrMetThrValAspProIleAs
0 -	s N315. stridium group; shylococcus.	i) equence update) nnotation update)	401 AA.		Serser	> ⋅	S H		TAGCCCTGAGTGTGAATTTG::: ;:: ;:: ;:: ;:: ;:: ;:: ;::	ACAAGGCCTGGGCTTGAAATT ::: ::::::::::::::::::::::::::::::::	CATTTAGACATCGAGGCCTTC ::: LeuArgGlyIleGluGluLeu	AGTCCCGAGGTATCTACGAGA ysSerArgGlyCysTyrGluT	ATTG ::: Vala	CAGACCTCCTTGGA ::: LeuIleIl	AGTTCAAAAAAGGGGTCCCTGTGA :: erValValLysGly	ırValAspProïleAspAlaPr
Kobayashi I., T., Kanamori M., Mizutani-Ui Y.,					1191 396	1149 380	1100 363	1050 346	1000 330	950 313	900 296	850 280	800 263	750 246	700	218

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SQ RET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to: Q99VC7 from: 1 to: 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "whole genome sequencing of meticillin-resistant Staphylococcus aureus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Complete proteome.
SEQUENCE 401 AA; 44455 MW; BAA35E9F6C6FD5A6 CRC64;
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EMBL; AP003132; BAB42061.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             110 ACATTGGCCAGAAGGAAGACTTCGAGGAAGCCAGGAAGAAGACTGAAG 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          210 GGAGTTCATCTGGCCGGCCATCCAGTCCAGCGCACTGTATGAGGACCGCT 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60 CCTCGTGTGGCTGAAGGAACAAGGCTATGACGTCATTGCCTATCTGGCCA 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   160 CTTGGGGCCAAAAAGGTGTTCATTGAGGATGTCAGCAGGAGTTTGTGGA 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18 aValGlnTrpLeuIleAspLysGlyTyrAspValValAlaCysCysLeuA 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  310 GAAATCGCCCAGCGGAGGGGGCCAAGTATGTGTCCCACGGCGCCCACAGG 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              52 MetGlyAlaValGluCysHisIleIleAspAlaThrLySGluPheSerAs 68
                                                                                                                                                                                                                                                                                                                                                                                                                   410 CCCAGATAAAGGTCATTGCTCCCTGGAGGATGCCTGAATTCTACAACCGG 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             360 AAAGGGGAACGATCAGGTCCGGTTTGAGCTCAGCTGCTACTCACTGGCCC 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          85 yrProLeuValSerAlaLeuSerArgProLeuIleAlaLysLysLeuVal 101
                                                                                                                                                                                                                                                                 510 CATCCCGGTCACTCCCAAGAACCCGTGGAGCATGGATGAGAACCTCATGC 559
                                                                                                                                                                                                                                                                                                                                       460 TTCAAGGGCCGCAATGACCTGATGGAGTACGCAAAGCAACACGGGATTCC 509
                                                                                                                                                                                                                                                                                                                                                                                135 roserLeuLysAlaPheAlaProValArgGluTrpAlaTrp...... 148
                                                                                                                                                                                       560 ACATCAGCTACGAGGCTGGAATCCTGGAGAACCCCAAGAACCAAGCGCCT 609
                                                                                                                                                                                                                              163 oValSerIleAsnHisAspSerProTyrSerIleAspGlnAsnLeuTrpG 180
                                                                                                                                                  180 lyargalaasnGluCysGlyIleLeuGluAspProTyrAlaalaProPro 196
||| ::: ::: ||| |||||||:::||||||||:::::
213 aAspGluIleIleLeuThrPheAspLysGlyIleProValGlnIle....
                                     660 TGACATTCTCGAGATCGAGTTCAAAAAAGGGGTCCCTGTGAAGGTGACCA 709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        spValGlyGluGlyLysAspLeuAspIleValTyrLysLysAlaLeuAsp 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACCTCCTGGGCACCTCTCTTGCCAGGCCCTGCATCGCCCGCAAACAAGTG 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pGluTyrValSerTyrAlaIleLysGlyAsnLeuMetTyrGluAsnAlaT 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                      yLysGlyAsnAspGlnValArgPheGluValAlaIleLysAlaLeuAsnP 135
                                                                                                                                                                                                                                                                                                    .....SerArgGluGluGluIleAspTyrAlaIleLysHisAsnilePr 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Quality:
                                                                            GluaspalaPheAspLeuThrAsnAlaLeuGluGluThrProAspThrAl 213
                                                                                                                 CCAGGTCTCTACACGAAGACCCAGGACCCAGCCAAAGCCCCCAACACCCC 659
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2.689
71.827
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seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       710 ACGTCAAGGATGGCACCACCACCAGACCTCCTTGGAGCTCTTCATGTAC 759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          760 CTGAACGAAGTCGCGGGCAAGCATGGCGTGGGCCGTATTGACATCGTGGA 809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          242 LeuAsnAlaLeuAlaGiyLysHisGlyIleGlyArgileAspHisValGl 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1010 GCATCGCCAAGTCCCAGGAGCGAGTGGAAGGGAAAGTGCAGGTGTCCGTC 1059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          258 uAsnArgLeuvalGiyIleLysSerArgGluIleTyrGluAlaProAlaA 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     810 GAACCGCTTCATTGGAATGAAGTCCCGAGGTATCTACGAGACCCCCAGCAG 859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1110 CAATGAGGAGCTGGTGAGCATGAACGTGCAGGGTGATTATGAGCCAACTG 1159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1060 CTCAAGGGCCAGGTGTACATCCTCGGCCGGGAGTCCCCACTGTCTCTCTA 1109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          275 laGluValIleLeuLysalaHisLysalaLeuGluThrIleThrLeuThr 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   860 GCACCATCCTTTACCATGCTCATTTAGACATCGAGGCCTTCACCATGGAC 909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   308 nLeuTyrAsnGlyLeuTrpPheSerProLeuThrAspSerLeuLysLeuP 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 960 GGTGTATACCGGTTTACGGCCTAGCCCTGAGTGTGAATTTGTCCGCCACT 1009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        292 LysAspValAlaHisPheLysProIleIleGluLysGlnPheAlaGluGl 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1160 ATGCCACCGGGTTCATCAACATCAATTCCCTC 1191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   325 heIleAspSerThrGinGlnTyrValSerGlyAspValArgIleLysLeu 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 342 PheLysGlyAsnAlaIleValAsnGlyArgLysSerProTyrThrLeuTy 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             358 raspGluLysLeuAlaThrTyrThrLysGluAspAlaPheAsnGlnAspA 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |||::::|||||||:::||| :::|||
375 laAlaValGlyPheIleAspIleTyrGlyLeu 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9KNT8;
01-CCT-2000 (TrEMBLrel. 15, Created)
01-CCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UNI-2001 (TrEMBLrel. 17, Last annotation update)
01-UNI-2001 (TrEMBLrel. 17, Last annotation update)
ARGININOSUCCINATE SYNTHASE (EC 6.3.4.5) (CITRULLINE--ASPARTATE
                                                                                                                                                             SEQUENCE FROM N.A.

STRAIN-EL TOR N16961 / SEROTYPE O1;

STRAIN-EL TOR N16961 / SEROTYPE O1;

STRAIN-EL TOR N16961 / SEROTYPE O1;

MEDLINE-20406833; PubMed=10952301;

Melson R.B.; Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,

Dedson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,

Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Sellers P.,

Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,

Gill S.R., Nelson K.E., Read T.D., Tettelin H., Dragoi I., Sellers P.,

Gill S.R., Nelson K.E., Read T.D., Tettelin H., Nierman W.C., White O.,

McDonald L., Utterback T., Fleishmann R.D., Nierman W.C., White O.,

Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9KNT8
                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=666;
                                                                                                                                                                                                                                                                                                                                                                                             Bacteria: Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               LIGASE).
                                         -i- PATHWAY: UREA CYCLE, PENULTIMATE STEP OF THE ARGININE BIOSYNTHETIC
                                                                                                                                             Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CGGGAAGTGCGCAAAATCAAACAAGGCCTGGGCTTGAAATTTGCTGAGCT 959
                                                                                                                      DNA sequence of both chromosomes of the cholera pathogen Vibrio
      PATHWAY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             404 AA.
                                                                                                                                                                                                                                           Sellers P.,
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alignment_block:
US-09-775-693-1 x Q9KNT8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Align seg 1/1 to: Q9KNT8 from: 1 to: 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ratio: 2.674 Percent Similarity: 71.320
610 CCAGGTCTCTACACGAAGACCCAGGACCCAGCCAAAGCCCCCAACACCCC 659
                                         187 isvalserThrGluGlyGlyValLeuGluSerThrTrpAsnAlaProAsn 203
                                                                 560 ACATCAGCTACGAGGCTGGAATCCTGGAGAACCCCAAGAACCAAGCGCCT 609
                                                                                                                        170 oCysalaAlaSerLeuThrLysIleTyrSerArgAspAlaAsnAlaTrpH 187
                                                                                                                                                                510 CATCCCGGTCACTCCCAAGAACCCGTGGAGCATGGATGAGAACCTCATGC 559
                                                                                                                                                                                                        154 LeuArgSerArgGluAlaCysLeuAspTyrLeuAlaGluArgAsnIlePr 170
                                                                                                                                                                                                                                               460 TTCAAGGGCCGCAATGACCTGATGGAGTACGCAAAGCAACACGGGATTCC 509
                                                                                                                                                                                                                                                                                     141 roAspLeuHisValileAlaProTrpArgGluTrpAsp...... 153
                                                                                                                                                                                                                                                                                                             410 CCCAGATAAAGGTCATTGCTCCCTGGAGGATGCCTGAATTCTACAACCGG 459
                                                                                                                                                                                                                                                                                                                                                                        124 yfysglyAsnAspGinValArgPheGiuGlyAlaPheAlaAlaLeuAlaP 141
                                                                                                                                                                                                                                                                                                                                                                                                              360 AAAGGGGAACGATCAGGTCCGGTTTGAGCTCAGCTGCTACTCACTGGCCC 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                   108 GluIleAlaArgLysValGlyAlaAspAlaLeuAlaHisGlyCysThrGl 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           310 GAAATCGCCCAGCGGGAGGGGCCAAGTATGTGTCCCACGGCGCCCACAGG 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          260 ACCTCCTGGGCACCTCTTTGCCAGGCCCTGCATCGCCCGCAAACAAGTG 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         210 GGAGTTCATCTGGCCGGCCATCCAGTCCAGCGCACTGTATGAGGACCGCT 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91 yrreuLeuGlyThrSerMetAlaArgProvalIleAlaLysAlaGlnVai 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        160 CTTGGGGCCAAAAAGGTGTTCATTGAGGATGTCAGCAGGGAGTTTGTGGA 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     113 TTGGCCAG...AAGGAAGACTTCGAGGAAGCCAGGAAGAAGGCCACTGAAG 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 74 sGlutyriletyrProThrLeuLysThrGlyAlaTyrTyrGluGlyLysT 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58 SerGlyAlaSerGluCysTyrIleValAspLeuLysGluGluPheValLy 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41 alGlyGlnGlyAspGluGluLeuLysGlyValGluAlaLysAlaLeuSer 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69 GCTGAAGGAACAAGGCTATGAC.....GTCATTGCCTATCTGGCCAACA 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25 pLeuLysGlu...AsnTyrAspCysGluValValAlaPheValAlaAspV 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00764; Arginosuc_synth; 1.

ProDom; PD003544; Arginosuc_synth; 1.

PROSITE; PS00564; ARGININOSUCCIN_SYN_1; 1.

PROSITE; PS00565; ARGININOSUCCIN_SYN_2; 1.

ATP-binding; Arginine biosynthesis; Complete proteome; Ligase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19 GTGGTTCTGGCCTACAGTGGCGGCCTGGACACCTCGTGCATCCTCGTGTG 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9 ValvalvalalaTyrSerGlyGlyLeuAspThrSerValIleIleProTr 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -! SIMILARITY: TO THE ARGININOSUCCINATE SYNTHASE FAMILY.
EMBL: AE004330; AAF95783.1;
TIGR; VC2642;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001518; Arginosuc_synth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBUNIT: HOMOTETRAMER (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           404 AA; 44465 MW; A65C73B442B5AF82 CRC64;
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OS
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ID Q9CC10 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_name: sp_bacteria:Q9CC10
Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R., Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D., Mungall K., Basham D., Brown D., Chillingworth T., Connor R., Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N., Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S., Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M., Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
                                                                                                                                                                                       MEDLINE=21128732; PubMed=11234002;
                                                                                                                                                                                                                                STRAIN-TN;
                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                       Mycobacterium leprae.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1160 ATGCCACCGGGTTCATCAACATCAATTCCCTC 1191
                                                                                                                                                                                                                                                                          Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium,
                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-2001 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1110 CAATGAGGAGCTGGTGAGCATGAACGTGCAGGGTGATTATGAGCCAACTG 1159
                                                                                                                                                                                                                                                                                                                                                                        ARGG OR ML1412
                                                                                                                                                                                                                                                                                                                                                                                   ARGINOSUCCINATE SYNTHASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-2001 (TrEMBLrel. 17, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9CC10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1060 CTCAAGGGCCAGGTGTACATCCTCGGCCGGGAGTCCCCACTGTCTCTCTA 1109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1010 GCATCGCCAAGTCCCAGGAGCGAAGTGGAAGGGAAAGTGCAGGTGTCCGTC 1059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    382 isAlaGlyGlyPheIleArgLeuTyrSerLeu 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          365 rSerGluAspPheAlaThrPheGlyAlaAspGluValTyrAspHisSerH 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        349 TyrLysGlyGlnalaValAlaThrGlnLysArgSerAlaAsnSerLeuTy 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      332 laAlaAspGluLeuAlaLysAspValAsnGlyGluValValIleLysLeu 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       315 uValTyrAspGlyArgTrpPheThrProLeuArgGlnAlaValPheAlaA 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               960 GGTGTATACCGGTTTACGGCCTAGCCCTGAGTGTGAATTTGTCCGCCACT 1009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        299 LysThrSerPheGluPheArgGluGluLeuGlyIleLysAlaSerHisLe 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                910 CGGGAAGTGCGCAAAATCAAACAAGGCCTGGGCTTGAAATTTGCTGAGCT 959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      282 lyThrileIleMetGluAlaLeuArgAlaValGluGlnLeuValLeuAsp 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 860 GCACCATCCTTTACCATGCTCATTTAGACATCGAGGCCTTCACCATGGAC 909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    265 uAsnArgLeuValGlyMetLysSerArgGlyCysTyrGluThrProGlyG 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             810 GAACCGCTTCATTGGAATGAAGTCCCGAGGTATCTACGAGACCCCAGCAG 859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   249 LeuAsnGlnLysGlyAlaLysHisGlyValGlyArgIleAspIleValGl 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             760 CTGAACGAAGTCGCGGGCAAGCATGGCGTGGGCCGTATTGACATCGTGGA 809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      236 ......AspGlyGluAla...MetThrProTyrAsnAlaLeuLeuTyr 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              710 ACGTCAAGGATGGCACCCACCCACCAGACCTCCTTGGAGCTCTTCATGTAC 759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    220 aGluTyrvalThrLeuGlnValAlaHisGlyGluValValAlaVal.... 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             660 TGACATTCTCGAGATCGAGTTCAAAAAAAGGGGTCCCTGTGAAGGTGACCA 709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     204 GluAspCysTrpValTrpThrValAspProGluGlnAiaProAsnGluAl 220
                                                                                                                                                                                                                                                                                                                                                                                          17, Last sequence update)
17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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US-09-775-693-1 x Q9CC10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity: 68.357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to: Q9CC10 from: 1 to: 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Massive gene decay in the leprosy bacillus.";
Nature 409:1007-1011(2001).
EMBL; AL583922; CAC30363.1; -.
Interpro; IPR001518; Arginosuc_synth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00764; Arginosuc_synth; 1.
probom; PD003544; Arginosuc_synth; 1.
pROSITE; PS00564; ARGININOSUCCIN_SYN_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          116 GCCAG...AAGGAAGACTTCGAGGAAGCCAGGAAGAAGGCACTGAAGCTT 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19 GTGGTTCTGGCCTACAGTGGCGGCCTGGACACCTCGTGCATCCTCGTGTG 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    163 GGGGCCAAAAAGGTGTTCATTGAGGATGTCAGCAGGGAGTTTGTGGAGGA 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69 GCTG...AAGGAACAAGGCTATGACGTCATTGCCTATCTGGCCAACATTG 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            213 GTTCATCTGGCCGGCCATCCAGTCCAGCGCACTGTATGAGGACCGCTACC 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22 pIleGlyLysGluThrSerHisGluValValAlaValValIleAspLeuG 39
                                                                                                                                                                                                                                                                                                                                                                                                                                  263 TCCTGGGCAGCTCTCTTGCCAGGCCCTGCATCGCCCGCAAACAAGTGGAA 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        56 GlyAlavalGluAlailevalvalAspAlaArgAspGluPheAlaGluGl 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  106 AlaalaArgalaHisGlyGlySerIleValalaHisGlyCysThrGlyLy 122
                                                                                                                                                                                                                                                                                                                                                                          313 ATCGCCCAGCGGGAGGGGGCCAAGTATGTGTCCCCACGGCGCCACAGGAAA 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                               72 yTyrCysLeuProThrValLeuAsnAsnAlaLeuTyrMetAspArgTyrP 89
                                                                                                                                                                                                                                                                                         363 GGGGAACGATCAGGTCCGGTTTGAGCTCAGCTGCTACTCACTGGCCCCCC 412
                                                                                                                                                                                                                                                                                                                                                                                                         89 roLeuValSerAlaIleSerArgProLeuIleValLysHisLeuValAla 105
                                                                                                                                                                                                                                 139 spLeuGluIleLeuAlaProvalArgAspTyrAlaTrpThr....... 152
                                                                                                                                                                                                                                                          413 AGATAAAGGTCATTGCTCCC......TGGAGGATGCCTGAA 447
                                                                                                                                                                                                    448 TTCTACAACCGGTTCAAGGGCCGCAATGACCTGATGGAGTACGCAAAGCA 497
                                                                                                                                                                      153 .....ArgGluLysAlaIleAlaPheAlaGluGl 162
                                                                                                               498 ACACGGGATTCCCATCCCGGTCACTCCCAAGAACCCGTGGAGCATGGATG 547
                                                                                    548 AGAACCTCATGCACATCAGCTACGAGGCTGGAATCCTGGAGAACCCCCAAG 597
                            598 AACCAAGCGCCTCCAGGTCTCTACACGAAGACCCAGGACCCAAGCCAAAGC 647
                                                       179 lnasnvalTrpGlyArgAlavalGluThrGlyPheLeuGluHisLeuTrp 195
Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         399 AA; 43915 MW; 3AD2B1D33EE50E7F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   685.50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        percent Identity: 37.440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps:
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seq_name: sp_archea:Q9UX31
    seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              648 CCCCAACACCCCTGACATTCTCGAGATCGAGTTCAAAAAAAGGGGTCCCTG 697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    698 TGAAGGTGACCAACGTCAAGGATGGCACCACCACCAGACCTCCTTGGAG 747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            229 alserIle.....AspGlySer..ProValSerMetLeuGlyA 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               798 TGACATCGTGGAGAACCGCTTCATTGGAATGAAGTCCCGAGGTATCTACG 847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 iaileGluala LeuAsnArgArgAlaGlyAlaGlnGlyValGlyArgLe 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           748 CTCTTCATGIACCTGAACGAAGTCGCGGGCAAGCATGGCGTGGGCCGTAT 797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            274 luAlaProGlyAlaMetValLeuIleThrAlaHisAlaGluLeuGluHis 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      848 AGACCCCAGCAGGCACCATCCTTTACCATGCTCATTTAGACATCGAGGCC 897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             898 TTCACCATGGACCGGGAAGTGCGCAAAATCAAACAAGGCCTGGGCTTGAA 947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1048 CAGGTGTCCGTCCTCAAGGGCCAGGTGTACATCCTCGGCCGGGAGTCCCC 1097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   948 ATTTGCTGAGCTGGTGTATACCGGTTTACGGCCTAGCCCTGAGTGTGAAT 997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       291 ValThrLeuGluArgGluLeuGlyArgPheLysArgGlnThrAspArgAr 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              307 gTrpAlaGluLeuValTyrAspGlyLeuTrpTyrSerProLeuLysThrA 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1098 ACTGTCTCTACAATGAGGAGCTGGTGAGCATGAACGTGCAGGGTGATT 1147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        998 TIGTCCGCCACTGCATCGCCAAGTCCCAGGAGCGAGTGGAAGGGAAAGTG 1047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1148 ATGAGCCAACTGATGCCACCGGGTTCATCAACATCAATTCCCTCAGGCTG 1197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             341 ArgMetValLeuHisGlyGlyHisIleAlaValAsnGlyArgArgSerAl 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      324 laLeuGluSerPheValAiaAlaThrGinGlnHisValThrGiyGluVai 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1198 AAGGAATATCATCGTCTCCAGAGCAAGGTCACTGCCAAA 1236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 357 aGluSerLeuTyrAspPheAsnLeuAlaThrTyrAspGluGlyAspThrP 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          374 heAspGlnSerAlaAlaArgGlyPheValTyrVal.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             386 .....TyrGlyLeuProSerLysLeuAlaAlaArg 395
                                                                                                                                                                                                                                                                                      01-MAY-2000 (TrEMBLrel. 13, Created) 01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update) ARGININOSUCCINATE SYNTHASE (EC 6.3.4.5).
STRAIN-DSM 1617 / P2; STRAIN-DSM 1617 / P2; STRAIN-DSM 1617 / P2; STRAIN-DSM 1617 / P2; STRAIN-DSM 1617 / Singh R.K., Chan-Weiher C.C.-Y., Allard G., Chow C., Charlebois R.L., Singh R.K., Duguet M., Erauso G., Faguy D., Confalonieri F., Curtis B., Duguet M., Jeffries A.C., Kozera C., Gasterland T., Garrett R.A., Gordon P., Jeffries A.C., Kozera C., Kushwaha N., Lafleur E., Medina N., Peng X., Penny S.L., She Q., Kushwaha N., Van Der Oost J., Young F., Zivanovic Y., Doollittle W.F., St Jean A., Yensen C.W.; Ragan M.A., Sensen C.W.; "Gene content and organization of a 281-kbp contig from the genome of the extremely thermophilic archaeon, Sulfolobus solfataricus P2.";
                                                                                                                                                                                                                                                                                                                                                                                         Q9UX3:
                                                                                                                                                                                                                                                   Sulfolobus solfataricus.
                                                                                                                                                                                                               NCBI_TaxID=2287;
                                                                                                                                                                                                                                    Archaea;
                                                                                                                                                                                                                                    Crenarchaeota; Sulfolobales; Sulfolobaceae; Sulfolobus.
                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                              406 AA.
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alignment_block:
US-09-775-693-1 x Q9UX31
209 ProGluAspAlaPheGluTrpThrLys......GlnIleTyrAsnLy 222
                                    607 CCTCCAGGTCTCTACACGAAGACCCAGGACCCAGCCAAAGCCCCCAACAC 656
                                                                   192 rpGlyArgSerIleGluGlyAspIleIleSerAspProSerLeuGluVal 208
                                                                                                      557 TGCACATCAGCTACGAGGCTGGAATCCTGGAGAACCCCAAGAACCAAGGG 606
                                                                                                                                        176 eProlleLysVal...GluSerAspLysTyrSerIleAspGluAsnLeuT 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_scores:
                                                                                                                                                                           507 TCCCATCCCGGTCACTCCCAAGAACCCGTGGAGCATGGATGAGAACCTCA 556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1 to: Q9UX31 from: 1 to: 406
                                                                                                                                                                                                              164 .....ArgGluAspGluIleLysTyrAlaLysGluLysGlyIi 176
                                                                                                                                                                                                                                              457 CGGTTCAAGGGCCGCAATGACCTGATGGAGTACGCAAAGCAACACGGGAT 506
                                                                                                                                                                                                                                                                               151 alLysileileAlaProAlaArgileTrpAsnMetThr ...... 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity: 68.274
                                                                                                                                                                                                                                                                                                              416 TAAAGGTCATTGCTCCC.....TGGAGGATGCCTGAATTCTACAAC 456
                                                                                                                                                                                                                                                                                                                                                 134 yAsnAspGlnValArgPheAspLeuAlaValLysAlaLeuTyrProAspV 151
                                                                                                                                                                                                                                                                                                                                                                                   366 GAACGATCAGGTCCGGTTTGAGGTCAGCTGCTGCTCACTGGCCCCCCAGA 415
                                                                                                                                                                                                                                                                                                                                                                                                                      118 AlaLysLysGluGlyAlaGluAlaValAlaHisGlySerThrSerLysGl 134
                                                                                                                                                                                                                                                                                                                                                                                                                                           316 GCCCAGCGGGAGGGGCCAAGTATGTGTCCCACGGCGCCACAGGAAAGGG 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           101 euSerThrAlaLeuAlaArgProLeuIleAlaGluLysValValGluVal 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               266 TGGGCACCTCTCTTGCCAGGCCCTGCATCGCCCGCAAACAAGTGGAAATC 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                216 CATCTGGCCGGCCATCCAGTCCAGCGCACTGTATGAGGACCGCTACCTCC 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84 rileAlaTyrAlaileLysLeuAsnGlyLeuTyrGluGlyValTyrProL 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     166 GCCAAAAAGGTGTTCATTGAGGATGTCAGCAGGAGGTTTGTGGGAGGAGTT 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       116 GCCAGAAGGAAGACTTCGAGGAAGCCAGGAAGAAGGCACTGAAGCTTGGG 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  68 AlaSerLysHisTyrThrIleAspAlaValArgClnPheAlaAsnAsnTy 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51 lyGinLysAspAspPheLysLysIleGluGluArgAlaTyrIleAlaGly 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34 pleurysglurhrphelysalaglurlerlerhrvalThrvalAspvalg 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          69 GCTGAAGGAACAA...GGCTATGACGTCATTGCCTATCTGGCCAACATTG 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19 GTGGTTCTGGCCTACAGTGGCGGCGCCTGGACACCTCGTGCATCCTCGTGTG 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18 IleValLeuAlaTyrSerGlyGlyLeuAspThrThrValSerIleArgTr 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001518; Arginosuc_synth.
Pfam; PF00764; Arginosuc_synth; 1
ProDom; PD003544; Arginosuc_synth; 1.
PROSITE; PS00564; ARGININOSUCCIN_SYN_1; UNKNOWN_1.
PROSITE; PS00565; ARGININOSUCCIN_SYN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE 406 AA; 46285 MW; 3956BABC9FCD4C12 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases. EMBL; Y18930; CAB57663.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Quality: 656.50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Identity: 39.594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length:
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us-09-775-693-1.rspt

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alignment_scores:
                                                                                                                                                                         seq_documentation_block:
ID     043348     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_name: sp_human:043348
                                                                                              Stoneking T., Langston Y., Ahrens C.;
Submitted (JAN-198) to the EMBL/GenBank/DDBJ databases.
EMBL; AC003989; AAB96328.1; ...
InterPro; IPR001518; Arginosuc_synth.
Pfam; PF00764; Arginosuc_synth; 2.
ProDom; PD003544; Arginosuc_synth; 1.
                                                                                SEQUENCE
                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                     O43348;
O4348;
O1-JUN-1998 (TrEMBLrel. 06, Created)
O1-JUN-1998 (TrEMBLrel. 06, Last sequence update)
O1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HYPOTHETICAL PROTEIN RG007J15.1 IN CHROMOSOME 7031 (FRAGMENT).
                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1157 CTGAT ......GCCACCGGGTTCATCAACATC 1182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1107 CTACAATGAGGAGCTGGTGAGCATGAACGTGCAGGGTGATTATGAGCCAA 1156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             382 eraspGluMetalaArgGlyPherleGluile 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1057 GTCCTCAAGGGCCAGGTGTACATCCTCGGCCGGGAGTCCCCACTGTCTCT 1106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  367 oTyrSerGluLysIleAlaSerTyrAsn...LysGlyTrpTyr...ProS 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   351 ValSerAsnGlySerPheArgIleValGlyArgGluSerGluTyrSerPr 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1007 ACTGCATCGCCAAGTCCCAGGAGCGAGTGGAAGGGAAAGTGCAGGTGTCC 1056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     334 ysvalAlaAspGluMetAsnLysTrpIleSerGlyGluAlaLysValGlu 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   317 pLeuValTyrGlnGlyLeuTrpPheGluProLeuArgGluThrLeuHisL 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    957 GCTGGTGTATACCGGTTTACGGCCTAGCCCTGAGTGTGAATTTGTCCGCC 1006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    301 ThrProMetGluLeuArgPheLysArgHisIleAspGlnLeuTrpSerAs 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     907 GACCGGGAAGTGCGCAAAATCAAACAAGGCCTGGGCTTGAAATTTGCTGA 956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    284 laAlaLeuGlyLeuIleTyrAlaHisIleAspLeuGluLysThrIleTyr 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   857 CAGGCACCATCCTTTACCATGCTCATTTAGACATCGAGGCCTTCACCATG 906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    267 eGluAsnArgValValGlyPheLysSerArgGluValTyrGluValProA 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     807 GGAGAACCGCTTCATTGGAATGAAGTCCCGAGGTATCTACGAGACCCCAG 856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    251 PheLeuAsnLeuLysPheGlySerHisGlyPheGlyArgValGluHisI1 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   757 TACCTGAACGAAGTCGCGGGCAAGCATGGCGTGGGCCGTATTGACATCGT 806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     239 snGlyGluLys.....MetGluLeuAsnLysLeuValAsp 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     657 CCCTGACATTCTCGAGATCGAGTTCAAAAAAAGGGGTCCCCTGTGAAGGTGA 706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      707 CCAACGTCAAGGATGGCACCACCCACCAGACCTCCTTGGAGCTCTTCATG 756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     222 sLysGluIleValSerIleGluPheSerAsnGlyValProThrAlaValA 239
          Quality: 604.50
                                                                     166 AA; 18967 MW;
                                                        26B6A3ADCFEBFFAD CRC64;
Length:
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185

b

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seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Align seg 1/1 to: 043348 from: 1 to: 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-775-693-1 x 043348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                  1182 CAATTCCCTCAGGCTGAAGGAATATCATCGTCTCCAGAGCAAGGTCACTG 1231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1082 TCGGCCGGGAGTCCCCACTGTCTCTACAATGAGGAGCTGGTGAGCATG 1131
                                                                                                                                                                                                                                                                                                                                                                                  1232 CCAAA 1236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1132 AACGTGCAGGGTGATTATGAGCCAACTGATGCCACCGGGTTCATCAACAT 1181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1032 AGTGGAAGGGAAAGTGCAGGTGTCCGTCCTCAAGGGCCCAGGTGTACATCC 1081
                 SEQUENCE FROM N.A.
                                                                                                                                                             01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
MEDLINE=20504483; PubMed=11016950;
                                                                                                             ARGG OR VNG2437G.
Halobacterium sp. (strain NRC-1)
                                                                                                                                                                                                                                                                                                                                              165 alLys 166
                                                                                                                                                                                                                                                                                                                                                                                                            148 eAsnTyrLeuArgLeuLysGluTyrHisTyrPheGlnSerLysValThrV 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Halobacterium
                                                                                       Archaea; Euryarchaeota; Halobacteriales; Halobacteriaceae
                                                                                                                                                   ARGININOSUCCINATE SYNTHETASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               115 euSerGlnGluSerLeuLeuSerLeuTyrLysGluGluLeuValSerVal 131
                                                           NCBI_TaxID=64091;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      982 AGCCCTGAGTGTGAATTTGTCCGCCACTGCATCGCCAAGTCCCAGGAGCG 1031
                                                                                                                                                                                                                                   29нм02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                932 AAGGCCTGGGCTTGAAATTTGCTGAGCTGGTGTATACCGGTTTACGGCCT 981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          882 TTTAGACATCGAGGCCTTCACCATGGACCGGGAAGTGCGCAAAATCAAAC 931
                                                                                                                                                                                                                                                      29HMQ2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  832 TCCCGAGGTATCTACGAGACCCCCAGCAGCACCATCCTTTACCATGCTCA 88:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         782 ATGGCGTGGGCCGTATTGACATCGTGGAGAACCGCTTCATTGGAATGAAG 831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     732 CCAGACCTCCTTGGAGCTCTTCATGTACCTGAACGAAGTCGCGGGCAAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             682 AAAAAAGGGGTCCCTGTGAAGGTGACCAACGTCAAGGATGGCACCACCCA 731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82 AsnProGluCysLysSerValHisHisCysIleThrLysSerGlnGluG1 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33 isGlyMetGlyCysIleAspIleMetGluAsnCysPheIleArgIleLys 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16 sGlnThrSerLeuGluLeuPheValTyrLeuAsnGluValThrGlyLysH 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 LysLysGlyValProValLysValThr...IleLysMetAlaProProHi 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pLeuAspIleGluAspPheThrMetAspArgGluValHisLysIle.... 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4.003
81.622
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                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                             396 AA.
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alignment_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-775-693-1 x Q9HMQ2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
                                              481 .....ATGGAGTACGCAAAGCAACACGGGATTCCCA 511
146 yLeuThrArgGluTrpGluIleGluTyrAlaAlaGluArgAspLeuProV 163
                                                                                                     136 ......HisAspValCysAlaProValArgGluLeuGl 146
                                                                                                                                                       454 AACCGGTTCAAGGGCCGCAATGACCTG.....
                                                                                                                                                                                                                                                          404 TGGCCCCCAGATAAAGGTCATTGCTCCCTGGAGGATGCCTGAATTCTAC 453
                                                                                                                                                                                                                                                                                                           117 sThrGlyLysGlyAsnAspGlnLeuArgPheGlu....................... 128
                                                                                                                                                                                                                                                                                                                                            354 CACAGGAAAGGGGAACGATCAGGTCCGGTTTGAGCTCAGCTGCTACTCAC 403
                                                                                                                                                                                                                                                                                                                                                                                                                 101 IleLeuSerValAlaGluAlaGluGlyCysAlaAlaLeuAlaHisGlyCy 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     304 CAAGTGGAAATCGCCCAGCGGGAGGGGGCCAAGTATGTGTCCCACGGCGC 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        254 ACCGCTACCTCCTGGGCACCTCTCTTGCCAGGCCCTGCATCGCCCGCAAA 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              204 TGTGGAGGAGTTCATCTGGCCGGCCATCCAGTCCAGCGCACTGTATGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      154 CTGAAGCTTGGGGCCCAAAAAGGTGTTCATTGAGGATGTCAGCAGGAGTT 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      107 CCAACATTGGCCAGAAGGAA...GACTTCGAGGAAGCCAGGAAGAAGGCA 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ng W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M., Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J., Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A., Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W., Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H., Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D., Ebhardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.; Peron Natl Acad Gci if C & 07.13176-1101170000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         85 ly...TyrProLeuGlyThrAlaLeuAlaArgProValIleAlaAspAla 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69 eAla...AlaLeuCysPheAspAlaValArgAlaAsnAlaThrTyrGlnG 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
EMBL; AE005124; AAG20519.1; ...
InterPro; IPR001518; Arginosuc_synth.
Pfam; PF00764; Arginosuc_synth; 1.
ProDom; PD003544; Arginosuc_synth; 1.
PROSITE; PS00564; ARGININOSUCCIN_SYN_1; UNKNOWN_1.
PROSITE; PS00565; ARGININOSUCCIN_SYN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  54 AlaAlaLeuGlyValGluHis...HisValValAspAlaThrAlaGluPh
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1156 ACTGATGCCACCGGGTTCATCAACATCAATTCCCTCAGGCTGAAGGAATA 1205
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                                                                                                                                                                                                                                                                                                                                                                                180 ArgSerValGluGlyGlyHisLeuGluGluProAspTyrGlnProProAl 196
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                                        1206 TCATCGTCTCCAGAGCAAGGTC 1227
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355 erAlaAspAlaAlaSerPheAsnThrGluThrValAlaGlyIleGluGln 371
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                                                                                                                                                                                                                                                                                                                                       322 LeuAspGluThrGlnSerAlaValSerGLyThrValThrIleAlaPheGl 338
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380 rHisGlyPheGlnSerArgLeu 387
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OM nucleic - nucleic search, using sw model
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SUMMARIES

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AC021496 Homo sapi AC003989 Human BAC AE001924 Deinococc L00081 Human argin AE005687 Caulobact AX192950 Sequence D16959 Human HepG2 AL034382 S.pombe c	3705 Homo 8693 Homo 2833 Homo 9046 Homo 1496 Homo 1496 Homo 84 Human a 4525 Homo	M36/08 NUCLEOTICE X12459 RAT MRNA fo M31690 MOUSE arrgin BC002074 Mus muscu K01845 Human arrgin AC004616 Homo sapi AC073582 Homo sapi AC011307 Homo sapi AC011307 Homo sapi	20017E0717	530 Human m 27126 Homo 19243 Homo 27153 Homo 25175 Homo 25175 Homo 198 Bovine 09550 Homo 03057 Homo	Description

ALIGNMENTS

FEATURES Source	MEDLINE	TITLE JOURNAL	AUTHORS	REFERENCE			ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	LOCUS	HSASD	RESULT 1
LOCATION WWALLIELS 11560 /organism="Homo sapiens" /db_xref="taxon:9606"	84015388	Sequence for number affilinosuccurate symmetric communication Nucleic Acids Res. 11 (18), 6505-6512 (1983)	BOCK, H.G., Su, T.S., O'BILEN, W.E. and because Chua	1 (bases 1 to 1560)	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; HOMO.	Eukaryota; Metazoa; Chordata; Craniata; Vertebidia, Eucereoscomit,	Homo sapiens	human.	synthetase.	x01630.1 GI:28871	X01630	Human mRNA for argininosuccinate synthetase.			

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ATGGAGTACGCAAAGCAACACGGGATTCCCCATCCCGGTCACTCCCAAGAACCCCGTGGAGC
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            Unpublished (2000)

2 (bases 1 to 1975)

Sugano,S., Suzuki,Y., Ota,T., Obayashi,
Shibahara,T., Tanaka,T. and Nakamura,Y.
                                                                                        Kawabata,A., Hikiji,T., Kobatake,N., Inagaki,H., Ikema,Y., Okamoto,S., Okitani,R., Ota,T., Suzuki,Y., Obayashi,M., Nishi,T., Shibahara,T., Tanaka,T., Nakamura,Y., Isogai,T. and Sugano,S.
                                                                                 NEDO human cDNA sequencing
                                                                                                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                  oligo capping; fis (full insert sequence). Homo sapiens human small intestine cDNA to mRNA, clone_lib:HSI
                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                     AK027126 1975 bp mRNA PRI 29-SEP-2000 Homo sapiens cDNA: FLJ23473 fis, clone HSI13532, highly similar to HSASD Human mRNA for argininosuccinate synthetase.
                                                                                                                                                                                                                           clone:HSI13532.
                                                                                                                                                                                                                                                                               AK027126.1 GI:10440175
                                                                                                                                                          (sites)
Submission
                                                                                                                                                                         Primates;
                                                                                                                                                                                    Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                 project
                             Obayashi, M.,
                                                                                                                                                                    Catarrhini; Hominidae;
                         Nishi, T., Isogai, T.,
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COMMENT

NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert International Trade and Industry of Biotechnology; cDNA library sequencing: Research Association for Biotechnology; cDNA library construction, 5 - 6 3'-end one pass sequencing: Departent of construction, 5 - 6 3'-end one pass sequencing: Departent of virology and Human Genome Center, Institute of Medical Science, virology and Human Genome Center.

University of Tokyo (partly supported by Science and Technology

JOURNAL

submitted (29-AUG-2000) to the DDBJ/EMBL/GenBank databases. Sumio Sugano, Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure Analysis, Human Genome Center: Laboratory of Genome Structure Analysis, Japan Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan Shirokane-dai, 1-6-1, Minato-ku, Tel:81-3-5449-5286, [E-mail:cdnaleims.u-tokyo.ac.jp, Tel:81-3-5449-5286]

FEATURES

Agency).

Location/Qualifiers /organism="Homo sapiens" /db_xref="taxon:9606" /clone="HSI13532"

source

ORIGIN

BASE COUNT

459 a

argininosuccinate synthetase,

/note="highly similar to HSASD Human mRNA for

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"cloning vector pME18SFL3"

/clone_lib="HSI"

misc_feature

/note=

RESULT 3 BC009243 BC009243 LOCUS DEFINITION RAGE:3010137, mRNA, complete cds. ACCESSION RECOUSTANT MC. REYWORDS SOURCE ORGANISM ACTESSION MC. ACTESSION REPERENCE I (bases 1 to 1595) REFERENCE SUMMITTE (Collection (MGC), Cancer Genomics Office, National Cancer Submitted (06-UUN-2001) National Institutes of Health, Mammalian Entitute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, NIH-MGC Project URL: http://mgc.nci.nih.gov Emali: cyapbs-remail.nih.gov Emali: cyapbs-remail.nih.gov DNA Library Preparation: Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) Annu Madan, Rachel Dickhoff, Jessica Fahey, Stephanie Ford, Juli Annu Madan, Rachel Dickhoff, Jessica Fahey, Stephanie Ford, Juli	Db 1082 CANGCGCTCCAGGTCTTACACGANGACCCAGGACCCAAGGCCCAAGGCCCAAGCCCCAAGGCCCAAGGCCCCAAGGCCCCAAGGCCCAAGGCCCCAAGACCCCCC

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                                                                                                                                                                                                                                                                602 AAGGAAGACTTCGAGGAAGCCAGGAAGAAGGCACTGAAGCTTGGGGCCAAAAAAGGTGTTC 661
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                                                                                                                       301 aaacaagtggaaatcgcccagcgggaggggccaagtatgtgtcccacggcgccacagga 360
                 421 gtcattgctccctggaggatgcctgaattctacaaccggttcaagggccgcaatgacctg 480
                                                    902 GTCATTGCTCCCTGGAGGATGCCTGAATTCTACAACCGGTTCAAGGGCCGCAATGACCTG 961
601 caagegeetecaggtetetaeaegaagaeecaggaeecageeaaageeeceaaeaeeeet 660
                                                                                                                                                           AAACAAGTGGAAATCGCCCAGCGGGAGGGGGCCAAGTATGTGTCCCCACGGCGCCACAGGA 841
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BASE COUNT
501 GTCATTGCTCCCTGGAGGATGCCTGAATTCTACAACCGGTTCAAGGGCCGCAATGACCTG 560
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                                                                                                                                                                                                                                                                361 aaggggaacgatcaggtccggtttgagctcagctgctactcactggccccccagataaag 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 321 GCACTGTATGAGGACCGCTACCTCGTGGGCACCTCTTGCCAGGCCCTGCATCGCCCGC 380
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4557336.
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NINSLRLKEYHRLOSKVTAK"
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/clone_lib="NIH_MGC_17"
/lab_host="DH10B-R"
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Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Coldge, S., Domino, M., Doyle, M., Ferreira, P., Fitzhugh, W., Gage, D.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          781 catggcgtggggcgtattgacatcgtggagaaccgcttcattggaatgaagtcccgaggt 840
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      721 99caccaccaccagacctccttggagctcttcatgtacctgaacgaagtcgcgggcaag 780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                741 GACATTCTCGAGATCGAGTTCAAAAAAGGGGTCCCTGTGAAGGTGACCAACGTCAAGGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 661 gacattotogagatogagitoaaaaaaggggitocotgtgaaggtgacoaaogtcaaggat 720
                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. lobases 1 to 180839 homo. Linton,L., Nusbaum,C. and Lander,E. Homo sapiens chromosome 17, Clone RP11-54103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       601 caagcgcctccaggtctctacacggaagacccaggacccagccaaagcccccaacacccct 660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           toccaggagcgagtggaagggaaagtgcaggtgtccgtcctcaagggccaggtgtacatc 1080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTGTATACCGGTTTCTGGCACAGCCCTGAGTGTGAATTTGTCCGCCACTGCATCGCCAAG 1100
                                                                                                                                                                                                                                               HTG; HTGS_PHASE1; HTGS_DRAFT.
                                                                                                                                                                                                                                                                     AC027153.1 GI:7331447
                                                                                                                                                                                                                                                                                          Homo sapiens chromosome 17 clone RP11-54103 map 17, WORKING DRAFT ACO27153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACCATGGACCGGGAAGTGCGCAAAATCAAACAAGGCCTGGGCTTGAAATTTGCTGAGCTG 1040
                                                                                                                                                                                                                                                                                                                                      AC027153
                                                                                                                   (bases 1 to 180838)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAAGCGCCTCCAGGTCTCTACACGAAGACCCCAGGGACCCAAGCCCAAAAGCCCCCAACACCCCT 740
                                                                                                                                                                                                                                                                                                                              180838 bp
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Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Olivar, T.M., Oliver, J., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J., Vassillev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Vassillev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., LaRocque, K., Lamacars, R., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., Meldrin, J., Meneus, L., Mihova, T., Miranda, C., Mlenga, V., Morrow, J., Miranda, C., Mlenga, M., Miranda, C., Mlenga, M., Mlenga, M., Mlenga, M., Mlenga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (28-MAR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,
Grand-Pierre,N., Grant,G., Hagos,B., Heaford,A., Horton,L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Young, G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NOTE: This is a 'working draft' sequence. It currently consists of 28 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chemistry: Dye-terminator Big Dye; 100% of re Assembly program: Phrap; version 0.960731 Consensus quality: 158974 bases at least Q40 Consensus quality: 169058 bases at least Q30 Consensus quality: 174233 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Quality coverage: 3.6 in Q20 bases; agarose-fp quality coverage: 3.6 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequencing vector: M13; M77815;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center project name: L5602
Center clone name: 541_0_3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: sequence_submissions@genome.wi.mit.edu
------ Project Information
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Insert size: 179000; agarose-fp Insert size: 178138; sum-of-contigs
                                                                                                                                                                                                                                                                               7265 913; contig of 1859 bp in length 9124 923; gap of 100 bp 9224 10641; contig of 1418 bp in length 10642 10741; gap of 100 bp 10742 11042 - 100 bp
                   11947 12046: gap of 100 bp 12047 12046: gap of 100 bp 12047 14424: contig of 3378 bp in length 14425 14524: gap of 100 bp 14525 17721: contig of 3197 bp in length 17722 17821: gap of 100 bp 17822 20638: contig of 2817 bp in length 20639 20738: gap of 100 bp 24567: contig of 3829 bp in length 20739 24567: contig of 3829 bp in length
                                                                                                                                                                                                                                          10742 11946: contig of 1205
11947 12046: gap of 100 b
                                                                                                                                                                                                                                                                                                                                                                                                                             3416 3515: gap of 100 bp
3516 5368: contig of 1853 bp in length
5369 5468: gap of 100 bp
5469 7164: contig of 1696 bp in length
7165 7264: gap of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1504 1603: gap of 100 bp
1604 3415: contig of 1812 bp in length
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416 1503: cc
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24667: gap of
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contig of 1088 bp in length
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92717 101894: contig of 9178 bp in length
101895 101994: gap of 100 bp
101995 118357: contig of 16363 bp in length
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138989 180838: cont
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85468 92616: cont
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72774 79925: contig of 7152 bp in length
79926 80025: gap of 100 bp
80026 85367: contig of 5342 bp in length
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                                              /note="assembly_fragment"
33531. .38145
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24668. .29147
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20739 .24567
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9224. .10641
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1504. .3415
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                                                                                                         /note="assembly_fragment"
29248. .33430
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7265. .9123
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                                                                                                                                                                                                                                                                                                                      /note="assembly_fragment"
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14525. .17721
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                   /note="assembly_fragment"
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55104: contig of 6448 bp in length
204: gap of 100 bp
59833: contig of 4629 bp in length
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38145: contig of 4615 bp in length
45: gap of 100 bp
43517: contig of 5272 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BASE COUNT
                                                                                                                                                                                                                     147491 AATGGGAACAATCAGGTCCGGTTTGAGCTCATTTGCTACTCACTAGCCCCCCAGATAAAG 147550
                                                                         147611 ATGGAATATGCAAAGCAACACAGGATTCCCCATCCCGGTCACACCCCAAGAACTCGTGGAGC
                                                                                                                                                147551 GTCATTGCTCCCTGGAGGATGCCCAAATTCTACAACCAGCTCAAGGGCCCTCAATGACCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 1161;
                   541 atggatgagaacctcatgcacatcagctacgaggctggaatcctggaggaaccccaagaac 600
                                                                                            481 atggagtacgcaaagcaacacgggattcccatcccggtcactcccaagaacccgtggagc 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 aaggaagacttcgaggaagccaggaagaaggcactgaagcttgggggccaaaaaggtgttc 180
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Local Similarity 93.7%;
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ATGGACGAGAACCTCATGCATATCAGCTACGAGTCTGGAATCCTGGAGAACCCTAAGAAC
                                                                                                                                                                                                                                                                                              AAACAAATGGAAATCACCCAGTGGAAGGGGGCCAAGTATATGTCCCCACAGCACCACGGGA 147490
                                                                                                                                                                     9tcattgctccctggaggatgcctgaattctacaaccggttcaagggccgcaatgacctg
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                                                                                                                                                                                                                                                                                                                   aaacaagtggaaatcgcccagcgggagggggccaagtatgtgtcccacggcgccacagga 360
                                                                                                                                                                                                                                                                                                                                                                       GCACTGTATGAGGACCGCTACCTTCTGGGCACCTCTC--GCCAGGCCCTGCATCGCCTGC
                                                                                                                                                                                                                                                                                                                                                                                          gcactgtatgaggaccgctacctcctgggcacctctcttgccaggccctgcatcgcccgc
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138989. .180838
/note="assembly_fragment"
135476 c 35898 g 54235 t
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118458. .138888
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92717. .101894
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80026. .85367
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101995, .118357
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72774. .79925
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55205. .59833
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43618. .48556
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REFERENCE
AUTHORS
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SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 γ
                                                                                                                                                                                                                                                                                                            REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Db 147910 CAGGGTGTGGGCTGTATTGACATCATGGAGAACCGCTTCATTGGAATGAAGTCCCCGAGGG 147969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Db 147850 GGCACCACCACCAGACCTCATTGGAGCTCTTCATGTACCTGAACGAAGTCGTGGGCAAG 147909
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                                                                                                                                                                                                                                                                 AUTHORS
TITLE
                                                                                                                                                                       TITLE
                                                                                                                                                 JOURNAL
                                                                                                                                                                                                                                                                                                                                                                           ORGANISM
                                                                                                                                                                                                                                        JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1201 gaatatcatcgtctccagagcaaggtcactgccaaatag 1239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1141 ggtgattatgagccaactgatgccaccgggttcatcaacatcaattccctcaggctgaag
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 961 gtgtataccggtttacggcctagccctgagtgtgaatttgtccgccactgcatcgccaag
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                          Center: Joint Genome Institute
Center Code: JGI
                                                                                  Direct Submission Submitted (07-MAR-2000) Production Sequencing Facility, DOE Joint Submitted (17-MAR-2000) Mitchell Drive, Walnut Creek, CA 94598, USA On Jul 18, 2000 this sequence version replaced gi:7711790.
                                                                                                                                                                                     2 (bases 1 to 165439)
DOE Joint Genome Institute.
Web site: http://www.jgi.doe.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HTG HOMO Sapiens chromosome 5 clone CTD-2081C10, SEQUENCE, 20 ordered pieces.
                                                                                                                                                                                                                                                                               1 (bases 1 to 165439)
DOE Joint Genome Institute.
                                                                                                                                                                                                                                      Unpublished
                                                                                                                                                                                                                                                              Sequencing of Human Chromosome
                                                                                                                                                                                                                                                                                                                         Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                  AC025175.3
                                                                           ·---Genome Center
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  GI:9256455
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BASE COUNT
                                                                                                                                                                                                                       FEATURES
                           Query Match
       Best Local Similarity
                                                                                                                                                                                                       source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Consensus quality: 151915 bases at least Q40
Consensus quality: 160797 bases at least Q30
Consensus quality: 160797 bases at least Q20
Consensus quality: 162485 bases at least Q20
Estimated insert size: 164720; agarose-fp estimation
Estimated insert size: 164720; agarose-fp estimation
Quality coverage: 4.55 in Q20 bases; agarose-fp estimation
Quality coverage: 4.56 in Q20 bases; sum-of-contigs estimation
* NOTE: This is a 'working draft' sequence. It currently
* consists of 20 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* This sequence will be replaced
* but he shinks formance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Summary Statistics
                                                                                               45132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center clone name: CITB-H1_2081C10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center Project Name: 658711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the accession number will be preserved.

1 774: contig of 774 bp in length
775 874: gap of unknown length
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154883
156599
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115177
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78133
82252
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875
21898
21998
26273
26273
                                                                                      /clone="CTD-2081C10"
/clone_lib="CalTech human BAC library D"
32811 c 33426 g 52152 t 1918 other.
                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                   1. .165439
                                                                                                                                               /chromosome="5"
                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                    154882: gap of unknown length
156598: contig of 1716 bp in length
156698: gap of unknown length
161013: contig of 4315 bp in length
161113: gap of unknown length
                                                                                                                                                                                                                           162823: contig of 1710 bp in length
162923: gap of unknown length
165439: contig of 2516 bp in length
       88.1%;
93.6%;
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Score 1091.4; DB 2; Length 165439; Pred. No. 7.3e-217;
                                                                                                                                                                                                                                                                                                                                                                                                         gap of contig
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gap of
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                    1021 teccaggagegagtggaagggaaagtgcaggtgteegteeteaaggggeeaggtgtacate 1080
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ATGTCCGGCAAAGGCTCCGTGGTTCTGGCCTACAGTGGGGGCCCTGGACACCTCCTGCATC 69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dennis, J.A., Healy, \dot{P}.J., Beaudet, A.L. and O'Brien, W.E. Molecular definition of bovine argininosuccinate synthetase
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                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="MSGKGSVVLAYSGGLDTSCILVMLKEQGYDVIAYLANIGQKEDF
EBARKALKLCAKKVFIEDISKEFVEEFIWPAIQSSALYEDRYLLGTSLARPCIARKQ
VEIAQREGAKYVSHGATGKGNDQIRFELTCYSLAPQIKVIAPWRMPEEYNRFQGRNDL
MEYAKQHGIPVPVTPKNPWSWDENLMHISYEAGILENPKNQAPPGLYTKTQDPAKAPN
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KSRGIYETPAGTILYHAHLDIEAFTMDREVRKIKQGLGLKFAELVYTGFWHSPECEFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /protein_id="AAA30388.1"
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                                                                                                                                                                                                                                                                                                                                                                                         Quality coverage: 4.4 in Q20 bases; agarose-fp
Quality coverage: 4.6 in Q20 bases;
NOTE: This is a 'working draft' sequence. It currently
* consists of 11 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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Birren,B., Linton,L., Nusbaum,C. and Lander,E.
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Center clone name: 382_M_14
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                                                                                        100 bp
4670: contig of 2872 bp
4671 4770: gap of 100 bp
4771 8967: contig of 8968 anco
                                                                                                                                                                                                                                         1 1698: contig of 1698 bp in length
1699 1798: gap of 100 bp
1799 4670: contig of 2872 bp in length
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121641 ACACTGTATGAGGACCGCTACCTCCTGGGAACCTCTCTCGCCAGGCCCTGCATCACCCAC 121700
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117365 117464: gap of 100 bp
117465 188356: contig of 70892 bp in length
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4771. .8967
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21156: contig of 8044 bp
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            HTG 22-DEC-2000 Homo sapiens chromosome 11 clone RP11-382M14 map 11q, WORKING SEQUENCE, 20 unordered pieces.
AP003057.1
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Published Only in DataBase (2000) In press 2 (bases 1 to 190665) Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hor Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
                                                                               20 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (20-DEC-2000) Masahira Hattori, The Institute of Physical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 190665)
Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujlyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y. Homo sapiens 190,665 genomic DNA of 11q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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preserved
                                                                                                                                                                                                                                          NOTE: This is a 'working draft' sequence. It currently consists of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens DNA, clone:RP11-382M14.
                                              as soon as it is available and the accession number
                                                                                                                                                                                                                                                                                                                  Chemistry: Dye-terminator ET-amersham; 100% of reads Assembly program: Phrap; version 0.990329
Consensus quality: 185978 bases at least 040
Consensus quality: 187598 bases at least 030
Consensus quality: 187598 bases at least Q30
Consensus quality: 188368 bases at least Q20
Insert size: 188765; sum-of-contigs
Quality coverage: 8.21x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center project name: HumDraftll Center clone name: RP11-382M14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: hattori@gsc.riken.go.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center code: RIKEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequencing vector: PCR products; 100% of reads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Web site: http://hgp.gsc.riken.go.jp/
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1 31506 contig of 31506 bp in length
31607 63890 contig of 27537 bp in length
63991 91527 contig of 27537 bp in length
91628 106175 contig of 14548 bp in length
106276 115509 contig of 9234 bp in length
115610 125111 contig of 9502 bp in length
113312 13211 contig of 9502 bp in length
125212 133211 contig of 9608 bp in length
142674 149569 contig of 6896 bp in length
149670 155266 contig of 5597 bp in length
155367 165212 contig of 5597 bp in length
165313 171081 contig of 5769 bp in length
165313 171081 contig of 5769 bp in length
174921 178093 contig of 3639 bp in length
178194 182424 contig of 3639 bp in length
18834 186908 contig of 4231 bp in length
183834 186908 contig of 4231 bp in length
189378 189277 contig of 3073 bp in length
189378 189277 contig of 1209 bp in length
189378 190655 contig of 1288 bp in length arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved. 31506: contig of 31506 bp in length

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FEATURES
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178094 178193: gap of
178194 182424: contig of
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171082 171181:
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187009 189277: contig of 2269
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183834 186908: contig of
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182425 182524:
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189378 190665: contig of 1288
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165313 171081: contig
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91628 106175: contig of 14548 bp in length
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63890: contig of 32284 bp in length
990: gap of 100 bp
91527: contig of 27537 bp in length
                                                                                                           .155266
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Pred. No. 6.1e-210;
0; Mismatches 85;
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                                                                                                                                                                                                                                                Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheters, R., McCarthy, M., McEwan, P., McGurk, A., Mranda, C., Mlenga, V., Morrow, J., Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Olivar, T.M., Oliver, J., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B., Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B., Rogov, P., Talamas, J., Talamas, J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Boguslavkiy, L., Boukhyalter, B., Brown, A., Burkett, G., Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodfo S. Domino M. Dovie M. Perreira D. Fitthinh W. Gare D. Dodfo S. Domino M. Dovie M. Perreira D. Fitthinh W. Gare D.
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Submitted (09-JUN-2000) Whitehead Institute/MIT Center Research, 320 Charles Street, Cambridge, MA 02141, USA
                                                                                      Direct Submission
                                                                                                                                                                       Tesfaye,S., Theodore,J., Tirrell,A., Travers,M., Trigilio,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 201989)
Birren, B., Linton, L., Nusbaum, C. and Lander, E.
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                                                                                                                                   Zainoun, J., Zimmer, A. and Zody, M.
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COMMENT
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Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     as soon as it is available and the accession number will be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequencing vector: M13; M77815; 100% of reads Sequencing vector: M13; M77815; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731 Consensus quality: 189508 bases at least Q30 Consensus quality; 195790 bases at least Q30 Consensus quality; 195790 bases at least Q30 Consensus quality; 198358 bases at least Q30
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Contact: sequence_submissions@genome.wi.mit.edu
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1276 1375: gap of 100 bp
1376 2986: contig of 1611 bp in length
2987 3086: gap of 100 bp
3087 4668: contig of 1582 bp in length
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4769 7645: cor
                               /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                           Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                319: gap of 100 bp

34818: contig of 8499 bp in length

918: gap of 100 bp

40947: contig of 6029 bp in length
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261: gap of 100 bp
26219: contig of 4958 bp in length
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ACACTGTATGAGGACCGCTACCTCCTGGGAACCTCTCTCGCCAGGCCCTGCATCACCCAC
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164645. .201989
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/clone_tib="RPCI-11 Human Male
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1376. .2986
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RESULT 10 AL353717/c

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AL353717

155019 bp

DNA 9 C

NA HTG clone RP11-562M8,

05-AUG-2001 SEQUENCING IN

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VERSION KEYWORDS

Homo sapiens chromosome 9 clone F PROGRESS ***, 3 unordered pieces. AL353717 AL353717.9 GI:15131977 HTG; HTGS_PHASE1; HTGS_ACTIVEFIN;

HTGS_ACTIVEFIN;

HTGS_DRAFT;

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                                             gtgtacatcctcggccgggagtccccactgtctctctacaatgaggagctggtgagcatg
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Chemistry: Dye-primer-amersham; 0% of reads
Chemistry: Dye-primer-amersham; 0% of reads
Consensus quality: 154590 bases at least Q40
Consensus quality: 154545 bases at least Q30
Consensus quality: 154709 bases at least Q20
Insert size: 154819; sum-of-contigs
Insert size: 154819; sum-of-contigs
Insert size: 15528; 7.3% error; agarose-fp
Quality coverage: 8.29x in Q20 bases; sum-of-contigs Quality
coverage: 7.89x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Assembly program: XGAP4; version 4.5
Sequencing vector: M13; M77815; 0% of reads
Sequencing vector: plasmid; L08752; 99% of reads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (04-AUG-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Aug 9, 2001 this sequence version replaced gi:15131481.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center project name: bA562M8
----- Summary Statistics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 155019)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                         42308
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117104 155019: contig of 37916 bp in length.
                                                                                                         Conservative
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97716 11700
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/note="assembly_fragment:01189
fragment_chain:1"
117104...155019
                                                                                                                                                                                                                                                  /note="assembly_fragment:02543
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a 31372 c 33444 g 47694 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="9"
                                                                                                                                                                                                                                                                                                                                                                                                                              /note="assembly_fragment:03117
fragment_chain:1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="RPCI-11.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="RP11-562M8"
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7715: gap of 100 bp
117003: contig of 19288 bp in length
                                                                                                                              85.4%;
                                                                                                                              Score 1057.8; DB 2
Pred. No. 6.9e-210;
                                                                                                       Mismatches
                                                                                                                                                       DB 2;
                                                                                                       87;
                                                                                                                                                                                                                                                       201 others
                                                                                                         Indels
                                                                                                                                                     Length 155019;
                                                                                                       6; Gaps
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Дb	61 65336	ctcgtgtggctgaaggaacaaggctatgacgtcattgcctatctggccaacattggccag 1	20 5277
Оy	121 65276	aaggaagacttogaggaagccaggaagaaggcactgaagcttggggccaaaaaggtgttc:	80 5217
Дy	181	atgtcagcagggagtttgtggaggag	40
	65216		5157
Qу	241 65156	gcactgtatgaggaccgctacctcctgggcacctctcttgccaggccctgcatcgcccgc 3	00 5097
Qy	301	aaatcgcccagcgggaggggg	60
Db	65096		5037
ОУ	361 65036	aaggggaacgatcaggtccggtttgagctcagctgctactcactggccccccagataaag 4	20 4977
Qy Db	421 64976	gaattotacaaccggtt GAGTTCTACAACCGGTT	80 4917
QУ	481 64916	tcccatcccggtcactccca	40 4857
Qу	541	9aacetcatgcacatcagctacgaggctggaatcctg	00
Дъ	64856		4799
Qy	601	gtctctacacgaagacccaggacccagccaaa	60
Db	64798		4739
Qу	661	ttcaaaaaaggggtccctgtgaaggtga	20
	64738		4679
Qу Дъ	721 64678	ctccttggagctcttcatgt CTCCTTGGAGCTTTTCGTGT	80 4619
Qy	781	gacatcgtggagaaccgcttcattggaat	40
Db	64618		4559
Qy Db	841 64558	tagac TAGAC	00 4499
Qy	901	gcgcaaaatcaaacaaggcctgg	60
Db	64498		4439
Qу	961	gtgtataccggtttacggcctagccctgagtgtgaatttgtccgccactgcatcgccaag 1	020
	64438		4379
Qy	1021	tcccaggagcgagtggaagggaaagtgcaggtgtccgtcc	080
Db	64378		4319
Qу	1081 64318	ctoggccgggagtccccactgtctctctacaatgaggagctggtgagcatgaacgtgcag 1	140 4259

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Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Banks,T., Barbaria,J.,
Benton,J., Bimage,K., Blanken,B.,
Benton,J., Bouck,J.,
Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C.,
Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C., Carron,T.F.,
Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R.,
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                                                                                                    Submitted (25-DEC-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One
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                                                                of Molecular and Human Genetics, Baylor Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                             Direct Submission
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                                                                                                                                                                                                                                                                              unpublished
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Worley,K.C.
Direct Submission
Direct Submission
Submitted (05-JUN-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Jun 1, 2001 this sequence version replaced gi:14190590.
INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email Direct Submission
Submitted (01-JUN-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA gc-help@bcm.tmc.edu (bases 1 to 159687)

CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are o sequenced and submitted once, so the sequence for the remainder the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing. are only

ANNOTATION OF FEATURES:

of a local database th local mapping efforts. STSs are identified using ePCR (Genome Res. 7:541-1 a local database that includes entries from dbSTS, 7:541-550) searches

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage. SEQUENCING READ COVERAGE: Sequencing is completed to a minimum

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation

QUALSTAT-REPORT----

200 180 160 # 140 bases 120 100 80	Distribution of Quality < 40 Bases	Position Original+Context	Contig length: Phrap values in estimate: Average error rate (BCM-Phrap estimate): Fraction of Phrap values less than 40: Number of consensus changing edits: Number of N's in consensus:
* * *	ses	Edited+Context	160224 159430 1.12363e-05 0.00137364

60 40 20

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FEATURES

Version:

1.01 qxfo

Location/Qualifiers

source

repeat_region

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/chromosome="12" organism="Homo sapiens"

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. 1974

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1985.

_family="L1ME1"

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complement(11501. .11569)
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complement(11571. .12240)
                                                                                                            complement(12242. .12407)
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                                                                            /rpt_family="AluSx"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            _family="MLT1-INTERNAL"
                                                      Score 1055.4; DB 9 pred. No. 2.2e-209;
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                                                                                                                                                                                                                             CACGGCGTGGGCCGTACTGACATCGTGGAGAACCGCTTTATTGGAATGAAGTCTCGAGGT
                                                                                                                                                                                                                                         caagcgcctccaggtctctacacgaagacccaggacccaggccaaagcccccaacacccct 660
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                                                                                                                                                                                    ATCTAGGAGGCCCCGGCAGGCACCATCCTTTACCACGCTCATTTAGACATCAAGGCCTTC
                                                                                                                                                                                                                                                                      GGCTCCACCTACCAGACCTCCTTGGAGCTCTTCATGTACCTGAACGAAGTCGCGGGCAAA
                                                                                                                                                                                                                                                                                 ggcaccacccaccagacctccttggagctcttcatgtacctgaacgaagtcgcggggcaag
                                                                                                                                                                                                                                                                                                                                                            CAAGCGCCTCCAGGTCTCTACGCGAAGACCCCAGGACCC-----GGCCCCCAACACCCCT
                                                                                                                                                                                                                                                                                                                                                                                                     ATGAACAAGAACCTCATGCACATCAGCTACGAGGCTGGAATCCTGGAGAATCCCAAGAAC
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Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H.,
Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C.,
Elhaj, C., Escotto, M., Falls, T., Ferragytto, D., Flagg, M., Ford, J.,
Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T.,
Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S.,
Hamilton, K., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A.,
Hernandez, J., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C.,
Hollins, B., Homsi, F., Howard, S., Huber, J., Hulyk, S., Hume, J.,
Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S.,
Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J.,
Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.,
Li, J., Liz, Lichtarge, O., Lieu, C., Liu, J., Liu, W.,
Lewis, L., Li, J., Liz, Lichtarge, O., Lieu, C., Liu, J., Liu, W.,
Loulseged, H., Lozado, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R.,
Ma, J., Maheshwari, M., Mapua, P., Martin, R., Martindale, A.,
Martinez, E., Massav, E., Maybiney, E., McLend, M. P., Meador, M.,
Martinez, E., Massav, E., Maybiney, E., McLend, M. P., Meador, M.,
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Martinez, E., Maybiney, E., McLend, M., Martinez, M.,
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                                                                                                                                               Submitted (22-MAR-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Jan 8, 2001 this sequence version replaced gi:12043803.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Thomas,S., Usmani,K., Vasquez,L., Vera,V., Villalon,D., Vinson,R. Wall,R., Wang,S., Ward.Moore,S., Warren,R., Washington,C., Watlington,S., Williams,G., Williamson,A., Wleczyk,R., Wooden,S., Williamson,A., Wleczyk,R., Wooden,S.,
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DNA HTG 08-JAN-2001
HTG 08-JAN-2001
HOMO sapiens chromosome 12 clone RP11-85503, WORKING DRAFT
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Center code: BCM
                                                              Center: Baylor College of Medicine
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Db 158350 ATTGAGGATGTCAGCAGGGAGTTTGTGGAGGAGTTCATCTGGCCCAGCCATCCAGTTCAGC 158291
                                                                                                                                                                                            Db 158469 CTCCTGTAGCTGAAGGAACAAGGCTATGATGTCATTGCCTACCTGGCCAACATTAGCCAG 158410
                                                                                                                                                                                                                                                                                           Db 158529 ATGTCCAGAAAAAGCTCTGTGGTTCTGGCCTACAGTGGTGGCCTGGACACCTCCTGCATC 158470
                                                                                                 Db 158409 AAGGAAGATTTCAAGGAAAACCAGGAAGAA-GCATTGAAGCTTTGGGGGCCAAAAAGGTGTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BASE COUNT
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                                                                                                                                                                                                                                                                                                                                                                                               Matches 1145;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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                    121 aaggaagacttcgaggaagccaggaaggaaggcactgaagcttggggccaaaaaggtgttc 180
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                                                                                                                                                                                                                      ctcgtgtggggggaacaaggctatgacgtcattgcctatctggccaacattggccag,120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               * NOTE: Estimated insert size may differ from sequence length

(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* consists of 8 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64581 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chemistry: Dye-primer Bodipy: 6% of reads
Chemistry: Dye-terminator Big Dye: 94% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 201671 bases at least Q40
Consensus quality: 204577 bases at least Q30
Consensus quality: 205669 bases at least Q30
Estimated insert size: 201838; sum-of-contigs estimation
Quality coverage: 9.7x in Q20 bases; sum-of-contigs estimation
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Center project name: H_DJ241P17.
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Waterston, R.H.
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                                                 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Fi (bases 1 to 1868)
Freytag, S.O., Bock, H.G., Beaudet, A.L. and O'Brien, W.E.
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                                                ATGAACAAGAACCTCATGCACATCAGCTACGAGGCTGGAATCCTGGAGAATCCCAAGAAC
                                                                                                                                                       ATGGAATACGCAAAGCACCACGGGATTCCCATCCTGGTCACTCCCAAGAACCTGTGGAGC
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                                                                                                                                                                                        Submitted (03-AUG-1999) Production Sequencing Facility, DOE Jo Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, On Aug 31, 2000 this sequence version replaced g1:7454179.
                                                                                                                                                                                                                                                             2 (bases 1 to 110716)
DOE Joint Genome Institute.
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DOE Joint Genome Institute.
                                                                                                                                                         Center: Joint Genome Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens chromosome
Consensus quality: 99834 bases at least Q40
                  Summary Statistics
                                                    Center clone name: CIT978SKB_87B2
                                                                                     Project Information
                                                                                                                        Web site: http://www.jgi.doe.gov
                                                                                                                                          Center Code: JGI
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241 gcactgtatgaggaccgctacctcctgggcacctctcttgccaggccctgcatcgcccgc
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                                                                              ATTGAGGATGTCAGCAGGAGTTTGTGGAGGAGTTCATCTGGGCGGCCATCCAGTCCAGC
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Consensus quality: 106925 bases at least Q30
Estimated insert size: 155000; pulse field gel estimation
Estimated insert size: 19416; sum-of-contigs estimation
Quality coverage: 8.72 in Q20 bases; pulse field gel estimation
Quality coverage: 8.72 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 14 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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/chromosome="5"
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22087: contig of 4360 bg

22187: gap of unknown le

31159: contig of 8972 bg

31259: gap of unknown le

40249: contig of 8990 bg

40349: gap of unknown le

55366: contig of 15017 k

55366: gap of unknown le

84335: contig of 28869 le

84435: gap of unknown le
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES	

Result)	Query	-	,	COLEMANTES	
No.	Score	Match	Match Length DB	DB 	ID	Description
	1232.6	99.5	1725	22	ААН72909	Human cervical can
N	1232.6	99.5	2810	22	AAH34821	Human colon cancer
ω	1232.6	99.5	2812	21	AAF16219	Human prostate can
4	466.8	37.7	969	22	AAI12589	Probe #2522 for ge
ψ	466.8	37.7	969	22	AAI33937	Probe #2623 used t
Φ	466.8	37.7	969	22	AAI02494	Probe #2485 used t
7	450.4	36.4	678	22	AAI21777	Probe #11710 for q
œ	450.4	36.4	678	22	AAI47060	Probe #15746 used
9	450.4	36.4	678	22	AAI07462	Probe #7453 used t
10	351.4	28.4	1048	21	AAF14080	Aspergillus oryzae
11	310.4	25.1	360	22	AAI28968	Colon tumour relat

New isolated nucleic acid for diagnosing and treating cervical cancer

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		44.	, 00	σ ω		2 9 9	10.9	$\frac{12.6}{11.6}$	13.4	16.5 13.4	17.5	18.3	18.5	22.5
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AAH13926 AAF71221 AAH68245 AAX55560	AAV13836 AAV05372 AAF91874 AAC58117	AAV52348 AAF12057 AAV52191	AAA81473 AAF21613 AAF91396	AAV74785 AAV75150	AAH52904 AAH54077	AAF/1920 AAH68528 AAX11829	AAH66511 AAH66512	AAH72308 AAH69430	AAZ80726 AAH71231	AAC34397 AAZ80429	AAI29308	AAC30247	AAA70071	AAC98292
ruman cuna sequenc Corynebacterium gl C glutamicum codin Viral-encoded sema		Streptococcus pneu Aspergillus oryzae Streptococcus pneu	N. meningitidis pa Neisseria meningit N. meningitidis (s	Staphylococcus aur Staphylococcus aur	S. epidermidis ope S. epidermidis gen	Corynebacterium gi C glutamicum codin Human biallelic po	C glutamicum codin	Human cervical can	Human colon cancer Human cervical can	Arabidopsis thalia Human colon cancer	tumour	Human secreted pro	ovarian	Human colon cancer

ALIGNMENTS

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RESULT
AAH72909
08-DEC-1999;
21-DEC-1999;
14-MAR-2000;
12-MAY-2000;
09-JUN-2000;
21-JUL-2000;
                WPI; 2001-375006/39.
                                                                                                                           08-DEC-2000; 2000WO-US33312
                                                                                                                                            14-JUN-2001.
                                                                                                                                                            WO200142467-A2
                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                              Cervical cancer;
                                                                                                                                                                                                              Human cervical cancer marker nucleic acid 4183.
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99US-0171350.
9200US-0189315.
2000US-0203791.
2000US-0210600.
2000US-0220114.
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99US-0163280.
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AAH32943 to AAH37195 and AAG73514 to AAG777788 represent human colon cancer associated nucleic acid molecules (N) and proteins (P), where the proteins are collectively known as colon cancer antigens. The colon cancer antigens have cytostatic activity and can be used in gene therapy and vaccine production. N and P may be used in the prevention,

useful

preventing,

3414-3415;

9803pp;

English.

colon and/or

cancer-associated polypeptides,
r treating colorectal cancers -

treating

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Matches 1235;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              present invention.

N.B. Pages 666 to 682 and page 7053 of the missing at time of publication, meaning no SEQ ID NO:1027 to 1052, 7921 and 7922.
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                         Prostate cancer associated gene sequences, referred cancer antigens, useful for treatment, prevention, a
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27-SEP-2000;
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
Probe; microarray;
                          Probe #2623
                                                                              AAI33937
                                                                                                       AAI33937 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                    atggacgagaacctcatgtgtatcagctatgaggctggaatcctggagaaac
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Pred. No. 6.9e-114;
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antenatal
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26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
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27-SEP-2000;
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ctcgtgtggctgaaggaacaaggctatgacgtcattgcctatctggccaaccattggccag
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                                                       aaggggaacgatcaggtccggtttgagctcagctgctactcactggccccccagataaag
                                                                                                  gcactgtatgaggaccgctacctcctgggcacctctctttgccaggccctgcatcgcccgc
                                                                                                                                                                                         gtcattgctccctggaggatgcctgaattctacaaccggttcaagggccgcaatgacctg
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; 2000US-0608408.
; 2000US-0632366.
; 2000US-0234687.
; 2000US-0234687.
; 2000US-0236359.
; 2000GB-0024263.
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Pred. No.
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No. 6.
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RESULT AAIOUT AAIO AAIO XX AAIO XX DT O9-C XX Prob XX Prob XX Prob XX Prob XX Prob XX Prob O9-1 XX O4-I PR 20-1 PR 20-
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30-JUN-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                        The present invention relates to novel single exon nucleic acid probes. The present sequence is one such probe. The probes are useful for measuring human gene expression in a human breast sample, where the prob hybridises at high stringency to a nucleic acid expressed in the human breast. The probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human breast, particularly those diseases with polygenic aetiology. The diseases include: breast cancer, disorders of development, inflammatory diseases of the breast, fibrocystic changes, proliferative breast disease and non-carcinoma tumours.
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                                                                                                                                                                                                                         Sequence 969
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2000US-0632366.
2000US-0234687.
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88.0%;
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Note: The sequence data for this patent did not form part of the prin specification, but was obtained in electronic format directly from WI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cttgtgtggctgaaggaacaaggacatgttgtcattgcctacctggccaacattggccag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               atgtccagcaaaggatccatggttctggcccacagtggtggcctggacacctcctgcatg 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         genome-derived single exon nucleic acid probes useful for zing gene expression in human cervical epithelial cells -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25; SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The
                                                                         standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             invention relates to human single exon nucleic acid probe present sequence is one such probe. The SENPs are derived
               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           No 11710; 487pp; English
                                                                        DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36.4%;
87.8%;
                                                                         678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
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Query Match
Best Local
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30-JUN-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to single exon nucleic acid probes (SENP). The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    04-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Probe #15746 used to measure
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   atgtccagcaaaggctccgtggttctggcctacagtggcggcctggacacctcgtgcatc 60
                                                                                        aaacaagtggaaatcgcccagcgggaggggccaagtatgtgtcccacggcgcccacagga
                                                                                                                                                                                                                                     aaggaagacttcgaggaagccaggaagaaggcactgaagctttggggccaaaaaggtgttc
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               aaggggaacgatcaggtccggtttgagctcagctgctactcactggccccccagataaag
                                                                                                                                                             gcactgtatgaggaccgctacctcctgggcacctctcttgccaggccctgcatcgcccgc
                                                                                                                                                                                                                aaggaagacttcgagaaagacaggaaggaaggcatgcaagcttggggccaaaaaggtgttc
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aaggagaacgatcaggtccagtttgagctcacctgct----cactggcccccagattaag
                                                                     aaacaagtggaaattacccagcaggaggggcccaagtacgtatcctatggcatcatggga
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2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0234687.
2000US-0236359.
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                      Query Match
  Matches
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26 - MAY - 2000;
30 - JUN - 2000;
03 - AUG - 2000;
                                                                                                                      The present invention relates to novel single exon nucleic acid probes. The present sequence is one such probe. The probes are useful for measuring human gene expression in a human breast sample, where the prob hybridises at high stringency to a nucleic acid expressed in the human breast. The probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human breast, particularly those diseases with polygenic aetiology. The diseases include: breast cancer, disorders of development, inflammatory diseases of the breast, fibrocystic changes, proliferative breast disease and
                                                         Sequence
                                                                                          specification,
                                                                                                     non-carcinoma tumours
Note: The sequence dat
                                                                                                                                                                                                                                          Claim
                                                                                                                                                                                                                                                                  Novel single exon nucleic in a human breast -
                                                                                                                                                                                                                                                                                                                                                                    04-OCT
                                                                                                                                                                                                                                                                                                                                                                              21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-JAN-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200157270-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Probe; human; breast disease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAI07462 standard;
                                                                                                                                                                                                                                                                                                                                              (MOLE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    inflammatory disease; proliferative breast disease; non-carcinoma tumour.
 ches 504;
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                                                                             ftp.wipo.int/pub/published_pct_sequences.
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                                                                                        The sequence data for this patent did not form floation, but was obtained in electronic format
             Similarity
                                                                                                                                                                                                                                                                                                                                              MOLECULAR
                                                          678
                                                                                                                                                                                                                                       SEQ ID No 7453; 322pp; English.
                                                                                                                                                                                                                                                                                                                       Hanzel DK,
  Conservative
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2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0234687.
2000US-0236359.
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          Score 450.4;
Pred. No. 1.3
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             1.3e-109;
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Gaps
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                              (NOVO)
                                                                                                                                                                                        Multiple gene expression; filamentous fungal cell; EST; expressed sequence tag; Fusarium venenatum; Aspergillus niger; Aspergillus oryzae; Trichoderma reesel; identification; recombination; culture condition; environmental stress; spore morphogenesis;
                                                               22-MAR-1999;
                                                                                      22-MAR-2000;
                                                                                                            28-SEP-2000
                                                                                                                                   WO200056762-A2
                                                                                                                                                        Aspergillus oryzae
                                                                                                                                                                               metabolic
                                                                                                                                                                                                                                              Aspergillus
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                                                                                                                                                                                                                                                                                                                  AAF14080 standard; cDNA; 1048
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gtcattgctccctggaggatgcccgagttctactactggctcaatggctgcaatgatctg
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                              NOVO
                                                                                                                                                                             pathway engineering;
                                                                                                                                                                                                                                              oryzae EST SEQ ID NO:6603
                              NORDISK BIOTECH NORDISK AS.
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                                                                 99US-0273623
                                           INC
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                                                                                                                                                                             catabolic
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                                                                                                                                                                             pathway engineering;
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Berka

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Rey

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Shuster

JR,

Kauppinen

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Clausen

ΙG,

Olsen PB;

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Monitoring differential expression of genes in filamentous fungal cells uses fluorescence-labeled nucleic acids isolated from the cells and a
                                                                                                                                                    Claim
                                                                                                                                                              substrate of expressed sequence tags -
                                                                                                                                                   88; Page 2701; 3161pp; English.
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engineering. Using ESTs provides several advantages over genomic or random cDNA clones including elimination of redundancy as one spot on an array equals one gene or open reading frame, and organisation of the microarrays based on function of the gene products to facilitate analysis of the results. AAF07478 to AAF1147 represents ESTs from Aspergillus Fusarium venenatum; AAF11248 to AAF11853 represents ESTs from Aspergillus oryzae; and AAF14879 to AAF14878 represents ESTs from Aspergillus oryzae; and AAF14879 to AAF15337 represents ESTs from Trichoderma reesei, which are discovered, possible functions of unknown open reading frames can be identified and gene copy number variation and stability can be monitored. The expression of genes can be used to study how FF cells adapt to changes in culture conditions, environmental stress, spore morphogenesis, recombination, metabolic or catabolic pathway in a first filamentous fungal (FF) cell relative to expression of genes same genes in one or more second filamentous fungal cells. Monitoring the global expression of genes from FF cells allows the production potential of the microorganisms to be improved. New genes may be discovered, possible functions of motors. expression of genes in a first filamentous fungal (FF) cell relative to expression of the same genes in one or more second filamentous fungal cells. The method uses fluorescence-labeled nucleic acids isolated from the FF cells and a substrate of expressed sequence tags (EST). The ESTs are used in the methods for monitoring differential expression of genes are used in the methods for monitoring differential expression of genes all specifically claimed invention describes a method for monitoring differential of genes in a first filamentous fungal (FF) cell relative to in the present invention.

Sequence 1048 BP; 196 A; 364 C; 251 G; 237 T; 0 other;

Query Match

Score

DB 21;

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cacgggattcccatcccggtcactcccaagaacccgtggagcatggatgagaacctcatg
                                                     atgcctgaattctacaaccggttcaagggccgcaatgacctgatggagtacgcaaagcaa 498
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                                 gateceaagttetteaagegtttegetggeegtaaegateteetegaetatgeegeeag
                                                                                                   cgtttcgaactggctttctatgccatccagccctccatcaagatcatcgccccttggcgt 507
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No. 2.5e-83;
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25; Page 273; 472pp; English.

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RESULT 3
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                                                                                                                                                             30-DEC-1999;
10-JAN-2000;
15-FEB-2000;
06-MAR-2000;
19-MAY-2000;
29-JUN-2000;
                                                                                         King
                               Colon tumor associated proteins and nucleic acids useful for prevention, diagnosis and treatment of colonic cancer -
                                                                                                                                                                                                                                                                                                                                                       Human; immunotherapy; diagnosis; colon cancer; colon tumour;
                                                                                                                                                                                                                                                                                                                                                                            Colon tumour related determined cDNA sequence for contig
                                                                   WPI; 2001-441847/47
                                                                                                                                                                                                                                               29-DEC-2000;
                                                                                                                                                                                                                                                                                              WO200149716-A2
                                                                                                                                                                                                                                                                                                                    Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAI28968 standard; cDNA; 360 BP
                                                                                                                                                                                                                                                                                                                                          immunogenic;
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                                                                                                    Lodes MJ,
                                                                                                                            CORIXA CORP
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                                                                                         Wang T,
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2000US-0480321.
2000US-0504629.
2000US-0519444.
2000US-0575251.
2000US-0609448.
                                                                                                                                                                                                                                                                                                                                          gene
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                                                                                                                                                    2000US-0649811
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                                                                                                                                                                                                                                                                                                                                          therapy; vaccine; colonic cancer; ss
                                                                                         Jiang
                                                                                                      Benson DR,
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RESULT 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCAP expression and activity. The anti-(I) antibodies may also be used as diagnostic agents for detecting the present TCAPs in samples (e.g. by enzyme linked immunosorbant assay (ELISA)). AAI28460 to AAI29512 and AAM24494 to AAM24523 represent nucleotide and amino acid sequences given in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     1058
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                  immunomodulatory; muscular; gynaecological; gastrointestinal;
nephrotropic; antiinfective; antibacterial; gene therapy; wound;
neural disorder; immune system disorder; muscular disorder;
                                                                                                                                                                                                                                                                                            AAC98292 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      expression, such as colonic cancer. For example, (I) and (II) may be
reproductive disorder; gastrointestinal disorder; renal disorder.
                                                                                     identification; cytostatic; cardioactive; neuroprotective; vulnerary;
                                                                                                                                                                                                                                                                                                                                                                                                         301
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                                                                                                                                                        colon cancer antigen nucleotide sequence SEQ ID NO:302
                                                                                                          colon cancer; colon cancer antigen; diagnosis; detection;
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95.5%;
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Pred. No. 1.2e-72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          103 G;
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                                                                                                                                                                                                               B
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      neuroprotective, immunomodulatory, gynaecological, gastrointestinal, vulnerary, nephrotropic, antiinfective and antibacterial activities, ar can be used in gene therapy. The colon cancer antigen polynucleotides, proteins and antibodies to the proteins are useful for the prevention, treatment and diagnosis of colon disorders, such as colon cancer. The polynucleotides may be used in diagnostics and research, such as for chromosome identification, and as hybridisation probes. The proteins may also be used to prevent diseases such as neural disorders, immune system disorders, muscular disorders, reproductive disorders gastrointestinal disorders, wounds, renal disorders, infectious diseases, and cardiovascular disorders. AAC98764 to AAC98772 and AAB5407 represent sequences used in the exemplification of the present inventor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAC97991 to AAC98763 encode the human colon cancer associated proteins, called human colon cancer antigens, given in AAB53234 to AAB54006. The human colon cancer antigens can have cytostatic, cardioactive, muscular;
                                                                                                       1026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Colon cancer associated gene sequences, referred to as colon cancer antigens, useful for the treatment, prevention, and diagnosis of co
                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 738; 2104pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rosen CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-MAR-2000; 2000WO-US05883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       infectious disease;
                                                                                                                                                                                                                                                                                                                      846
                                                                       189
 249
                                                                                                                                                                                                                 69
                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                ggaccgggaagtgcgcaaaatcaaacaaggcctgggcttgaaatttgctgagctggtgta
                                                                                                                                                                                                                                                                                                   cgagaccccagcaggcaccatcctttaccatgctcatttagacatcgaggccttcaccat 905
                                                                                     ggagcgagtggaagggaaagtgcaggtgtccgtcctcaagggccaggtgtacatcctcgg
                                                                                                                                                           taccggtttacggcctagccctgagtgtgaatttgtccgccactgcatcgccaagtccca
ccgggagtccccactgtctctctacaatgaggagctggtgagcatggatgagaa
                                  ccgggagtccccactgtctctctacaatgaggagctggtgagcatgaacgtgca
                                                                                                                                          taccggtttctggcacagccctgagtgtgaatttgtccgccactgcatcgccaagtccca
                                                                                                                                                                                                              ggaccgggaagtgcgcaaaatcaaacaaggcctgggcttgaaatttgctgagntggtgta
                                                                                                                                                                                                                                                                                 cgagaccccagcaggcaccatcctttaccacgctcatttagacatcgaggccttcaccat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000-587534/55
                                                                   ggagcgagtggaagggaaagtgcaggtgtccgtcctcaagggccaggtgtacatcctcgg
                                                                                                                                                                                                                                                                                                                                                        284;
                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                such as colon cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ruben SM
                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                            B₽;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-0124270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cardiovascular disorder;
                                                                                                                                                                                                                                                                                                                                                                       22.5%;
96.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                          A; 126 C;
                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                         Pred.
                                                                                                                                                                                                                                                                                                                                                                                       Score 278.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                            115 G;
                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                         No.
                                                                                                                                                                                                                                                                                                                                                                                                                                            78
                                                                                                                                                                                                                                                                                                                                                                         .2e-64;
                                                                                                                                                                                                                                                                                                                                                                                                                                            T; 5 other
                                                                                                                                                                                                                                                                                                                                                                                       DB 21;
                                                                                                                                                                                                                                                                                                                                                        10;
                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                       Length 440;
                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             present
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                                                                                                         1085
                                                                                                                                            188
                                                                                                                                                                                                                                                  965
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and

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AAA70071/c ID AAA70071 standard; cDNA; 234

ВP

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RESULT 14
AAC30247
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Best Local
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17-DEC-1998;
23-JUN-1999;
24-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                               The present invention describes an isolated polypeptide comprising an immunogenic portion of an ovarian carcinoma protein (or its variants). Ovarian carcinoma proteins, and polypucleotides encoding them, have cytostatic activity and can be used in gene therapy and vaccines ovarian carcinoma polypeptides, nucleic acids, antibodies and vaccines are useful for the prevention, diagnosis and treatment of cancer, preferably ovarian cancer. AAA69691 to AAA70077 and AAB12552 to AAA112557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 18; Page 194; 299pp; English.
                                                                                                                                                                                                                                                                                                                Sequence 234 BP; 47 A; 63 C; 63 G; 61 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cancer, preferably ovarian cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Immunogenic portion of an ovarian carcinoma protein and the nucleic acid encoding it, useful for the diagnosis, prevention and treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mitcham JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200036107-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tumour antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-NOV-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human ovarian carcinoma antigen polynucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAA70071;
                                                                         842
                                                                                                  114
                                                                                                                                                   174
                                                                                                                                                                                                                                                     Local Sir
hes 231;
                                                54
                                                                                                                                                                                                                                                                                                                                         resent human ovarian carcinoma polynucleotides and proteins used in exemplification of the present invention.
                                                           tctacgagaccccagcaggcaccatcctttaccatgctcatttagacatcgagg
                                                                                                                                              TCTACGAGACCCCAGCAGGCACCATCCTTTACCACGCTCATTTAGACATCGAGG
                                                                                                            atggcgtgggccgtattgacatcgtggagaaccgcttcattggaatgaagtcccgaggta
                                                                                              ATGGCGTGGGCCGTATTGACATCGTGGAGAACCGCTTCATTGGAATGAAGTCCCGAGGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000-431589/37.
                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      King GE,
                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98US-0216003.
99US-0338933.
99US-0404879.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    carcinoma; ovarian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98US-0215681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99WO-US30270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    identification; cytostatic; gene therapy; vaccine;
                                                                                                                                                                                                                                                               18.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Algate
                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                              Score 229.2; DB Pred. No. 3e-51;
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                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cancer; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Frudakis
                                                                                                                                                                                                                                                                           DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID
                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                          Length
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                                                                                                                                                                                                                                                                            234;
                                                                                                                                                                                                                                                  0;
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                                                                                                                       841
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ΧX

AAC30247 standard; cDNA;

270

RESULT 15 AAI29415/c ID AAI29415

standard;

cDNA;

222

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Best Local
                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                     mRNAs encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer CDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures
                                                                                                                                                                                                                                                                                                                Sequence 270 BP; 59 A; 72 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence is one of a large number of 5' ESTs derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dumas Milne Edwards
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-FEB-2000; 2000EP-0200610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-SEP-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human secreted protein 5' EST,
   220
                             181
                                                                                        121
                                                                                                                    100
                                                          160
                                                                                                                                                 61
                                                                                                                                                                              40
                                                                                                                                                                                                                                                      Local Similarity
             aaggaagacttcgaggaagccaggaaggcactgaagctttggggccaaaaaggtgttc
                                                                                                                                ctcgtgtgggtgaaggaacaaggctatgacgtcattgcctatctggccaacattggccag
                                                                                                                                                                                           atgtccagcaaaggctccgtggttctggcctacagtggcggcctggacacctcgtgcatc 60
aaggaagacttcgaggaagccaggaaggaaggcactgaagcttggggccaaaaaggtgttc
                                                                                                               ctcgtgtggctgaaggaacaaggctatgacgtcattgcctatctggccaacattggccag
                                                                                                                                                                           atgtccagcaaaggctccgtggttctggcctacagtggcggcctggacacctcstscatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; SEQ ID 34322; 71pp + CD-ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5' EST;
                                                                                                                                                                                                                                                                                                                                              and secretion
                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  chromosome mapping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99US-0122487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  expressed
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                                                                                                                                                                                                                                                    18.3%;
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                                                                                                                                                                                                                                                                                                                                              vectors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mapping; ss.
                                                                                                                                                                                                                                      2;
                                                                                                                                                                                                                                                    Score
Pred.
                                                                                                                                                                                                                                                                                                                83 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO: 34322
                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                      No.
                                                                                                                                                                                                                                                                                                                54 T; 2 other;
                                                                                                                                                                                                                                                                227.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Giordano
                                                                                                                                                                                                                                                      1.1e-50;
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                                                                                                                                                                                                                                                                     DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4
                                                                                                                                                                                                                                                                  21;
                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                  Length 270;
267
                           228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cDNA isolation;
                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                     Gaps
                                                                                     180
                                                                                                                    159
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В
                                                                                                                                                             The present invention describes colon tumour associated proteins (I) and CI the polynucleotides (II) that encode them. (I) have cytostatic activity. (I) and (II) can be used in gene therapy and vaccine production. (I) and CII) may be used in the prevention, diagnosis and treatment of diseases C associated with inappropriate colon tumour associated protein (TCAP) and CII) may be used to treat disorders associated with decreased expression by crectifying mutations or deletions in a patient's genome that affect the C rectifying mutations or deletions in a patient's genome that affect the patients own production of them. Additionally, (II) may be used to produce the TCAP proteins, by inserting the nucleic acids into a host cell culturing the cell to express the protein. (II) and its complementary sequences may also be used as DNA probes in diagnostic polymerase chain reaction (PCR) and hyporidisation assays to detect and therefore which patients may be in need of restorative therapy. (I) may also be used as antigens in the production of antibodies against TCAPs
                                                                                     Query Match
Best Local Similarity
                                                                       Matches 222;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-JAN-2000; 2000US-0480321.

15-FEB-2000; 2000US-0504629.

06-MAR-2000; 2000US-0519444.

19-MAY-2000; 2000US-0575251.

29-JUN-2000; 2000US-0609448.

28-AUG-2000; 2000US-0649811.
                                                                                                                                                                                                            and in assays to identify modulators of TCAP expression and activity. Anti-(I) antibodies and antagonists may also be used to down regulate TCAP expression and activity. The anti-(I) antibodies may also be used as diagnostic agents for detecting the presence of TCAPs in samples (e.g. by enzyme linked immunosorbant assay (ELISA)). AAI28460 to AAI29512 and AAM24494 to AAM24523 represent nucleotide and amino acid sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Χu J,
                                                                                                                                                           Sequence 222 BP; 31 A; 49 C; 76 G; 66 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 2; Page 400; 472pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-441847/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-DEC-1999;
10-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-DEC-2000; 2000WO-US35596
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; immunotherapy; diagnosis; colon cancer; colon tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Colon tumour related determined cDNA sequence for clone R0097:C02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              immunogenic; gene therapy; vaccine; colonic cancer; ss
, Lodes MJ,
GE, Wang T,
                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                            exemplification of the present invention.
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, Jiang Y;
                                                                                     17.9%;
100.0%;
                                                                       0;
                                                                     Score 222; DB 22;
Pred. No. 2.4e-49;
0; Mismatches 0;
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                                                                                                      DB 22; Length 222;
                                                                       Indels
                                                                       0;
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Search completed: February 12, 2002, 13:12:38 Job time: 1811 sec

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Minimum DB
Maximum DB
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Maximum Match 100%
Listing first 45 summaries
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
  seq length:
seq length:
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Copyright (c) 1993 - 2000 Compugen Ltd
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LILI LI	out the seq 4403765; 36; Gap	IN MYCOBACTERIUM	Sequence 1, Appli Sequence 1, Appli Sequence 3, Appli Sequence 4, Appli Sequence 45, Appl Sequence 14, Appl	7,

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                                                                                                                                                                Sequence 513, Application US/09328111 Patent No. 6262333 GENERAL INFORMATION:
              APPLICANT: Endege, Wilson O.
APPLICANT: Steinmann, Kathleen E.
APPLICANT: ASLIe, Jon H.
APPLICANT: Burgess, Christopher C.
APPLICANT: Bushnell, Steven E.
APPLICANT: Carroll III, Eddie
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; ORGANISM: Homo sapiens US-09-328-111-810
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                                                               SEQ ID NO 810
LENGTH: 175
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                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/328,111
CURRENT FILING DATE: 1999-66-08
EARLIER APPLICATION NUMBER: US 60/088,801
EARLIER FILING DATE: 1998-06-10
                                                                                                                                                                                                                                     TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION TITLE OF INVENTION: PRODUCTS FILE REFERENCE: CCD-257 (US)
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EARLIER FILING DATE: 1998-06-10
NUMBER OF SEQ ID NOS: 850
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 513
LENGTH: 175
                                                                                                                                    NUMBER OF SEQ ID NOS: 850
                                                                                                                                                                                                                                                                                                                 APPLICANT: Lewis, Marcia E. APPLICANT: Monahan, John E. APPLICANT: Schlegel, Robert
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APPLICANT: Carroll III, Eddie
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APPLICANT: Ford, Donna M.
APPLICANT: Lewis, Marcia E.
APPLICANT: Monahan, John E.
APPLICANT: Monahan, John E.
APPLICANT: Schlegel, Robert
TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
TITLE OF INVENTION: PRODUCTS
FILE REFERENCE: CCD-257 (US)
CURRENT APPLICATION NUMBER: US/09/328,111
CURRENT FILING DATE: 1999-06-08
CURRENT FILING DATE: 1999-06-08
                                            TYPE: DNA
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                                                                                                                                                                                                                Matches 122;
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INFORMATION FOR SEQ ID NO: 5:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 2277 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)343-4341
TELEFAX: (415)343-4342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              122 gctgaaggaatatcatcgtctccagagcaaggtcactgccaaatag 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62 cgtgcagggtgattatgagccaactgatgccaccgggttcatcaacatcaattccctcag 121
                                                                                                                                                                       516 ggtcactcccaagaacccgtggagcatggatgagaacctcatgcacatcagctacgaggc 575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 268 Bush Sci
CITY: San Francisco
                                                                                                                                          576 GGACAAGTACAAGGACACCCAGAGCGTGAGCGCCATCGGCGAGGAGAAGAGCCCACGAGAG 635
                                                                                                      576 tggaatcctggagaaccccaagaaccaagcgcctccaggtctctacacgaagacccagga 635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
696 GAACGACGACGACGACGACGACGACGACGAGGACGCGTGTTCGACGACGACGACGA
                                 636 cccaqccaaagcccccaacacccctgacattctcgagatcgagttcaaaaaaggggtccc 695
                                                                     636 CAAGCACCAGGAGAGCGTGAAGAAGAAGGACGCCGCGAGGAGGAGGACATGGAGGAGGAGGA 695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: UCB96-055
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                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/676,967
                                                                                                                                                                                                                               Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Osman Ph.D., Richard A
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                                                                                                                                                                                                                                                                                                                                                                                            2277 base pairs
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                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Floppy disk
                                                                                                                                                                                                                                                                                                                         CDNA
                                                                                                                                                                                                                                                                                                                                                         double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%;
                                                                                                                                                                                                                               3.3%; Score 40.4; DB 1; Length 2277; 47.3%; Pred. No. 0.031;
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hes 0;
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INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              756 GGAGGAGGAGAACATCGAGAGCAAGGTGACCAAGCCCGTGCAGATCCAGAAGCGCGCCGT 815
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          756 gtacctgaacgaagtcgc 773
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LENGTH: 2277 base pair
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                                                                                                                                                                                                                                                                                      576 GGACAAGTACAAGGACACCCAGAGCGTGAGCGCCATCGGCGAGGAGAAGAGCCACGAGAG 635
                                                                                                                                                                                                                                                                                                             516 ggtcactcccaagaacccgtggagcatggatgagaacctcatgcacatcagctacgaggc 575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                   696 tqtqaaqqtqaccaacgtcaaggatggcaccaccaccagacctccttggaqctcttcat 755
                                                                                                                                          696 GAACGACGACGACGACGACGACGACGACGAGGAGGACGCGTGTTCGACGACGAGGACGA 755
                                                                                                                                                                          636 cocaqeeaaageeeccaacaceeetgacattetegagategagtteaaaaaaggggteee 695
                                                                                                                                                                                                                 636 CAAGCACCAGGAGAGCGTGAAGAAGAAGGGCCGCGAGGAGGAGGACATGGAGGAGGAGGA 695
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/676,974
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816 GAAGCGCCCCCCCCCCC 833
                                                                   756 GGAGGAGGAGAACATCGAGAGCAAGGTGACCAAGCCCGTGCAGATCCAGAAGCGCGCCGT 815
                                756 gtacctgaacgaagtcgc 773
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TOPOLOGY: lir
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268 Bush Street, Suite 3200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2277 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (415)343-4342
(415)30 TN NO: 5:
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US-09-181-706-1
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Sequence 1, Application US/09181706 Patent No. 6130068 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 2277 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: UC:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)343-4341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Osman Ph.D., Richard A
REGISTRATION NUMBER: 36,627
                                                                                                                        816 GAAGCGCCCCGCCCCCCC 833
                                                                                                                                                                                   756 GGAGGAGAACATCGAGAGCAAGGTGACCAAGCCCGTGCAGATCCAGAAGCGCGCCGT 815
                                                                                                                                                                                                         696 tgtgaaggtgaccaacgtcaaggatggcaccacccaccagacctccttggagctcttcat 755
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Human Telomerase NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
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SOFTWARE: Patenti
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268 Bush Street, Suite 3200
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IBM PC compatible
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Sequence 1, Application US/09458791
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                                                                                   743 ACTACCCCTACAACTATACGAGCGGCGCTGCCCACCGGCTGGCCCAGCATGGCGCGCA 799
                                                                                                         245 tgtatgaggaccgctacctcctgggcacctctcttgccaggccctgcatcgcccgca 301
                                                                                                                                                          683 GCGCGGGCAGCCTGCACTTCGTGGACGCCTTTCTCTGGAACGGCAGCATCTACTTCCCCT 742
                                                                                                                                                                                                                                  623 AGGACACGGAGGGGCGCAGCCTGGCCACGCAGGAGCTGGGGCCGCCTCAAGCTGTGCGAGG 682
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HYPOTHETICAL: NO
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ATTORNEY/AGENT INFORMATION:
NAME: Henry, Janis C
REGISTRATION NUMBER: 34,3
                                                                                                                                                                                 FEATURE:
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APPLICATION NUMBER: --to be assigned-- (USSN 08/958,598

APPLICATION NUMBER: conversion to Provisional application)
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CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Janis C. Henry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                  watch 3.2%; Score 39.4; DB 3; Length 4707; Local Similarity 51.4%; Pred. No. 0.091; Pred. No. 0.091; Onservative 0; Mismatches 86; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 08/958,598 (converted to a APPLICATION NUMBER: Provisional, see below)
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OPERATING SYSTEM: PC-DOS/MS-DOS
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COMPUTER: II
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CITY: Seattle
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NUMBER OF SEQUENCES:

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GENERAL INFORMATION:
APPLICANT: Spriggs, Melanie
APPLICANT: SPRIGGS VIRAL ENCODED SEMAPHORIN PROTEIN
TITLE OF INVENTION: VIRAL ENCODED SEMAPHORIN PROTEIN
Sequence 1, Application US/09459066
Patent No. 6187909
GENERAL INFORMATION:
APPLICANT: Spriggs, Melanie
TITLE OF INVENTION: VIRAL ENCODI
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Best Local :
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SEQUENCE CHARACTERISTICS:
LENGTH: 4707 base pairs
                                                                                                                                                                                                                       245 tgtatgaggaccgctacctcctgggcacctctcttgccaggccctgcatcgcccgca 301
                                                                                                                                                                                                                                                                            683 GCGCGGGCAGCCTGCACTTCGTGGACGCCTTTCTCTGGAACGGCAGCATCTACTTCCCCT 742
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FILING DATE: 28-0CT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Henry, Janis C
REGISTRATION NUMBER: 34,347
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OPERATING SYSTEM: MS-DOS/Windows 95
SOFTWARE: Word for Windows 95, 7.0a
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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Similarity 51.4%;
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ZIP: 98101
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STRANDEDNESS: double
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LOCATION:
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      VIRAL ENCODED SEMAPHORIN PROTEIN RECEPTOR DNA AND POLYPEPTIDES
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US-09-459-066-1
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; APPLICANT: FLEISCHMAN, Robert D.
                                                                                                                                                                                        ; Sequence 2, Application US/09103840A ; Patent No. 6294328
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APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
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SOFTWARE: Word for Windows 95, 7.0a
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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ADDRESSEE: Janis C. |
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LENGTH: 4707 base pairs
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LOCATION:
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REGISTRATION NUMBER: 34.
REFERENCE/DOCKET NUMBER:
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Similarity 51.4%;
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; LENGTH: 204
; TYPE: DNA
; ORGANISM: Human
US-09-221-298-66
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; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2
                  Sequence 2, Application US/07951715A Patent No. 5625136
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Xu, Jiangchun
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY AND DIAGNOSIS
TITLE OF INVENTION: OF COLON CANCER
FILE REFERENCE: 210121.471
CURRENT APPLICATION NUMBER: US/09/221,298
CURRENT FILING DATE: 198-12-23
                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 112
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 66.
                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patent No. 628424
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver.
     APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 4403765
                                                                                                                                                            168 caaaaaggtgttcattgaggatgtcagcagggagtttgtggaggag 213
                                                                                                                                                                                                                                  140 ccaggaagaaggcactgaagcttggggccaaaaaggtgttcattgaggatgtcagcaggg 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        260 acctcctgggcacctctcttgccaggccctgcatcgcccgcaaac 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                200 agtttgtggaggagttcatctggccggccatccagtccagcgcactgtatgaggaccgct 259
                                                                                                                                       86 ggaacagagcatctctgaagagcccggctgggaggaggaggaagag 131
                                                                                                                                                                                                           26 ctataaagtccatcagttagagcaggagcaggcccggagggacgccctgaagcagcgggc 85
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Koziel, Michael G
                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                         Score 37.2; DB 4; Length 204; Pred. No. 0.075;
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Pred. No. 1
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; NAME/KEY: misc_feature
; LOCATION: 1.3468
; OTHER INFORMATION: /prod
; OTHER INFORMATION: optim
; OTHER INFORMATION: /note
US-07-951-715A-2
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                                                                                                                                                      Query Match 3.0%;
Best Local Similarity 49.0%;
Matches 99; Conservative
                                                                                                                                                                                          Query Match
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                            1060 ctcaagggccaggtgtacatcctcggccgggagtccccactgtctctctacaatgaggag 1119
                                                                                                  1000 gtccgccactgcatcgccaagtcccaggagcgagtgggaaggggaaagtgcaggtgtccgtc 1059
2545 GCCCTGGCCCGCGTGAAGCGCGCGAGAAGAAGTGGCGCGACAAGCGCGAGAAGCTGGAG 2604
                                                                          2485 GACGGCCACGCCCTGGGCAACCTGGAGTTCCTGGAGGAGAAGCCCCTGGTGGGCGAG 2544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: SPILLII, W. MULTAY
REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: S:
                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: other nucleic acid DESCRIPTION: /desc = "Synthetic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFORMUNICATION INFORMATION:
TELEPHONE: (919)541-8615
TELEFAX: (919)541-8689
                                                                                                                                                                                                                                                                                                                                                              FEATURE:
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TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING
TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
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OPERATING SYSTEM: PC-DOS/MS-DOS
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Lewis, Kelly S.
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Launis, Karen L.
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                                                                                                                                                                                                                                                       /product= "Full-length pure maize
optimized synthetic Bt"
/note= "Disclosed in Figure 3 as syn1T.mze"
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                                                                                                                                                  Score 37.2; DB 1; Length 3468; Pred. No. 0.35; O; Mismatches 103; Indels 0
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                                                                                                                                                                                                                         TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 4:
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REFERENCE/DOCKET NUMBER: S-18805/A/CGC 1577/CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8615
TELEFAX: (919)541-677
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TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
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APPLICANT:
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CORRESPONDENCE ADDRESS:
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                                                                                            MOLECULE TYPE:
DESCRIPTION:
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                                                         FEATURE:
                                                                        HYPOTHETICAL:
                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Hawthorne
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/07/951,715A FILING DATE: 25-SEP-1992
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   OTHER INFORMATION:
                                                                                                                              TOPOLOGY:
                                                                                                                                              STRANDEDNESS: single
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                                  NAME/KEY: misc_feature
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                     COCATION:
                                                                                                                                                           nucleic acid
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                                                                                          other nucleic acid
/desc = "Synthetic DNA"
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/product= "Full length synthetic
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Best Local :
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                                  CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 07/951,715
FILING DATE: 25-SEP-1992
                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 5859336artis Corporation
STREET: Patent & Trademark Dept., 520 White Plains
STREET: Rd., POB 2005
                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Dunder, Erik M.
APPLICANT: Pace, Gary M.
APPLICANT: Suttie, Janet L.
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
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PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                        CURRENT APPLICATION DATA:
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OTHER INFORMATION:
                                                                                                                 APPLICATION NUMBER: FILING DATE: 02-JU
                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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CITY: Tarrytown
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                                                                                                                                                                                                                                                                                              USA
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Launis, Karen L.
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/note= "Disclosed in Figure 3 as synful.mod. This sequenc
identical to flsynbt.fin as disclosed in Figure 1."
  US 07/772,027
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Pred. No. 0.35;
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FILING DATE: 04-OCT-1991 ATTORNEY/AGENT INFORMATION:

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Best Local S
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                               APPLICANT: Pace, Gary M.
APPLICANT: Suttie, Janet L.
TITLE OF INVENTION: SYNTHET
TITLE OF INVENTION: INSECTI
                                                                                                      APPLICANT:
APPLICANT:
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                     CORRESPONDENCE ADDRESS
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OTHER INFORMATION: /proc
OTHER INFORMATION: /proc
OTHER INFORMATION: /note
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LENGTH: 3468 base pair
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TELEFAX: (919)541-8689
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   ADDRESSEE:
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STRANDEDNESS: single
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                                                                                                                    Dawson, John L.
Dunder, Erik M.
                                                                                                                                                    Rothstein, Steven J. Bowman, Cindy G.
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5859336artis Corporation
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                                               SYNTHETIC DNA SEQUENCE HAVING ENHANCED INSECTICIDAL ACTIVITY IN MAIZE
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optimized synthetic Bt"
/note= "Disclosed in Figure 3 as synlT.mze"
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Best Local Similarity 49.0%;
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2665 AGCCAGTACGACCGCCTGCAGG
                                                                     1180 atcaattccctcaggctgaagg 1201
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DESCRIPTION:
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REFERENCE/DOCKET NUMBER: CG
TELECOMMUNICATION INFORMATION:
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OTHER INFORMATION: /proc OTHER INFORMATION: /note OTHER INFORMATION: identification identification in the control of the control o
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ATTORNEY/AGENT INFORMATION: NAME: Pace, Gary M.
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PRIOR APPLICATION DATA:
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PRIOR APPLICATION NUMBER: US 07/951,715
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IBM PC compatible
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ALIGNMENTS

FEATURES REFERENCE AUTHORS TITLE KEYWORDS SOURCE ORGANISM RESULT BI256461 COMMENT ACCESSION VERSION DEFINITION LOCUS JOURNAL source Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 878)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC Plate: LLAM11276 row: o column: 22 High quality sequence stop: 835. Location/Qualifiers cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: Incyte Genomics, Inc. DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov 602974488F1 NIH_MGC_12 Homo sapiens BI256461.1 GI:14810890 mRNA sequence. human. /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5113965"
/clone_lib="NIH_MGC_12"
/tissue_type="cervical carcinoma cell line"
/lab_host="DH10B" 1. .878 878 ďď Homo sapiens cDNA clone IMAGE:5113965 5', mRNA 17-JUL-2001 can be

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                                                  AGCATGGAGTGGGCCGTATTGACATCGTGGAGACCCGCTTCATTGGAATGACGTCCCGAG
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Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.4 kb. Library prepared by Life
Technologies."
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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BI258834
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Plate: LLAM11264 row: k column: 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1999)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/clone="IMAGE:5109251"
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602976921F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:5116133 5',
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Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                                                                                                  Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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National Institutes of Health, Mammalian Gene Collection (MGC)
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High quality sequence stop: 810.
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                                                                                                                                                                                                                                              DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information
                                                                                                                                                                                                                                                                            cDNA Library Preparation: Life Technologies, Inc.
/note="Organ: cervix; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.4 kb. Library prepared by Life
                                                  /tissue_type="cervical carcinoma cell line"
/lab_host="DH10B"
                                                                             /clone="IMAGE:5116133"
/clone_lib="NIH_MGC_12"
                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
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             mRNA sequence.
BI257913
                                  HI257913 875 bp mRNA EST 17-JUL-200: 602970844F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:5110307
 BI257913.1 GI:14813752
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TITLE
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481 atggagtacgcaaagcaacacgggattcccatcccggtcactcccaagaacccgtggagc 540
                                        440 GTCATTGCTCCCTGGAGGATGCCTGAATTCTACAACCGGTTCAAGGGCCGCAATGACCTG 499
                                                           421 gtcattgctccctggaggatgcctgaattctacaaccggttcaagggccgcaatgacctg 480
                                                                                                                                       361 aaggggaacgatcaggtccggtttgagctcagctgctactcactggccccccagataaag 420
                                                                                                                    380 AAGGGGAACGATCAGGTCCGGTTTGAGCTCAGCTGCTACTCACTGGCCCCCCAGATAAAG 439
                                                                                                                                                                                                                  301 aaacaagtggaaatcgcccagcgggagggggccaagtatgtgtcccacggcgccacagga 360
                                                                                                                                                                                            320 AAACAAGTGGAAATCGCCCAGCGGGAGGGGGCCAAGTATGTGTCCCACGGCGCCCACAGGA 379
                                                                                                                                                                                                                                                                        260 GCACTGTATGAGGACCGCTACCTCCTGGGCACCTCTTGCCAGGCCCTGCATCGCCCGC 319
                                                                                                                                                                                                                                                                                            241 gcactgtatgaggaccgctacctcctgggcacctctcttgccaggccctgcatcgcccgc 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 atgtccagcaaaggctccgtggttctggcctacagtggcggcctggacacctcgtgcatc 60
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Plate: LLAW11267 row: g column: 12
High quality sequence stop: 871.
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1 (bases 1 to 875)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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cDNA Library Arrayed by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.
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Plate: LLAM11263 row:
                                                                                                                                                                                                                                                                                                                                                                                              Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                               found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
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Clone distribution: MCC clone distribution information can be
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         /note="Organ: cervix; Vector: pCMV-SPORT6; Site_1: Not1; Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT Average insert size 1.4 kb. Library prepared by Life Technologies."

236 c 232 g 143 t
                                                                                            /tissue_type="cervical carcinoma cell line"
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                                                                                                                                /clone="IMAGE:5108729"
/clone_lib="NIH_MGC_12"
                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
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Query Match

Local Similarity

63.0%;

Score 780.6; DB 11 Pred. No. 3.7e-176;

DB 11;

Length 815;

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RESULT
BE379161
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601238137F1 NIH_MGC_44 Homo
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                                                                                                                                           BE379161.1 GI:9324526
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                                                               Craniata; Vertebrata; Euteleostomi;
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Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM265 row: j_column: 09
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Tissue Procurement: ATCC
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Contact: Robert Strausberg,
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/lab_host="DH10B (phage-resistant)"
/note="Organ: uterus; Vector: pOTB7; Site_1: XhoI; Site_2:
/note="Organ: uterus; Vector: pOTB7; Site_1: XhoI; Site_2:
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/clone_lib="NIH_MGC_44"
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BG828136
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Tissue Procurement: ATCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1999)
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National Institutes of Health, Mammalian
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Location/Qualifiers
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              /tissue_type="rhabdomyosarcoma"
//lab_host="DHIOB (phage-resistant)"
/lab_host="DHIOB (phage-resistant)"
/note="organ: muscle; Vector: pOTB7; Site_1: EcoRI;
Site_2: XhoI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the provided by closed for the state of the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
a 265 c 253 g 160 t
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/db_xref="taxon:9606"
/clone="IMAGE:4906132"
/clone_lib="NIH_MGC_17"
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Homo sapiens cDNA clone IMAGE:4906132
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               tatctacgagaccccagcaggcaccatcctttacca
                                                                      gcatggcgtgggccgtattgacatcgtggagaaccgcttcattggaatgaagtcccgagg
                                                                                                                                                                                                                               ccaagcgcctccaggtctctacacgaagacccaggacccagccaaagcccccaacacccc
                                                                                                                                                                                                                                                                                           CATGGATGAGAACCTCATGCACATCAGCTACGAGGCTGGAATCCTGGAGAACCCCCAAGAA
                                                                                                                                                                                                                                                                                                         catggatgagaacctcatgcacatcagctacgaggctggaatcctggagaaccccaagaa
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                                                                                                                TGGCACCACCAGA----CTCCTTGGAGCTCTTCATGTACCTGAACGAAGTCGCGGGCAA
                                                                                                                                                                          TGACATTCTCGAGATCGAGTTCAAAACAAGGGGTCCTGTGAAGGTGACCAACGTCAAGGA
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                                                        GCATGGCGTGGGCCGTATTGACATCGTGGAGAACCG-TTCATGGGAATGAAGTCCC-AGG
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RESULT BI259920

DEFINITION

mRNA sequence. BI259920

BI259920 918 bp 602968961F1 NIH_MGC_12

Homo

sapiens cDNA clone

IMAGE:5108463

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421 CAGCCACCAGACCTCCTTGGAGCTCTTCATGTACCTGAACGAAGTCGCGGGCAAGCATGG 480
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                  726 caccaccagacctccttggagctcttcatgtacctgaacgaagtcgcgggcaagcatgg 785
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                                                                                      666 tetegagatogagiteaaaaaaggggiteeetgtgaaggtgaeeaaegteaaggatggeae 725
                                                                        361 TCTCGAGATCGAGTTCAAAAAAGGGGTCCCTGTGAAGGTGACCAACGTCAAGGATGGCAC
                                                                                                                                     301 GCCTCCAGGTCTCTACACGAAGACCCAGGACCCAGCCAAAGCCCCCAACACCCCTGACAT 360
                                                                                                                                                                                                     241 TGAGAACCTCATGCACATCAGCTACGAGGCTGGAATCCTGGAGAACCCCCAAGAACCAAGC 300
                                                                                                                                                                                                                        546 tgagaacctcatgcacatcagctacgaggctggaatcctggagaaccccaagaaccaagc 605
                                                                                                                                                                                                                                                                                        486 gtacgcaaagcaacacgggattcccatcccggtcactcccaagaacccgtggagcatgga 545
                                                                                                                                                                                                                                                                      181 GTACGCAAAGCAACACGGGATTCCCCATCCCGGTCACTCCCAAGAACCCCGTGGAGCATGGA 240
                                                                                                                                                                                                                                                                                                                                       121 GCCTCCTGGAGGATGCCTGAATTCTACAACCGGTTCAAGGGCCGCAATGACCTGATGGA 180
                                                                                                                                                                                                                                                                                                                                                           427 g-ctccctggaggatgcctgaattctacaaccggttcaagggccgcaatgacctgatgga 485
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Plate: LLAM11262 row: j column: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: Incyte Genomics, Inc. DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.
Email: ggapbs r@mail.nih.gov
Tissue Procurement: ATCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Organ: Cervix; Vector: pcMV-SPORT6; Site_1: NotI; Site_2: Sali; Cloned unidirectionally. Primer: Oligo dr. Average insert size 1.4 kb. Library prepared by Life
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="cervical carcinoma cell line"
/lab_host="DH10B"
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      721 CAGGAGCGAGTGGAAGGGAAAGTGCAAGGTGTCCGTCCAAGGGCCAGGTGTACAATCC 780
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                                                                                                                                                                                                                  High quality sequence stop: 766.
                                                                                                                                                                                                                                           found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
plate: LLCM262 row: n column: 09
                                                                                                                                                                                                                                                                                                                                                                       Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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                                                                                                                                                                                                                                                                                   CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                    NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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/tissue_type="endometrium, adenocarcinoma cell line"
/lab_host="BH10B (phage resistant)"
/note="norgan: uterus; Vector: porB7; Site_1: XhoI; Site_2:
ECORI; cDNA made by oligo-dT priming Directionally adaptor: EGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of
                                                                                                                                /db_xref="taxon:9606"
/clone="IMAGE:3609032"
/clone_lib="NIH_MGC_44"
                                                                                                                                                                                 /organism="Homo sapiens"
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20-JUN-2001

BASE COUNT 용 δ 밁 δõ Q В Ş QΥ 밁 QΥ 밁 δÃ В Query Match 밁 Ş 밁 Š 밁 δÃ Q 망 Qy 밁 밁 QY В 24 Pocar 447 507 tcccatcccggtcactcccaagaacccgtggagcatggatgagaacctcatgcacatcag 566 181 ATTCTACAACCGGTTCAAGGGCCGCAATGACCTGATGGAGTACGCAAAAGCAACACGGGAT 61 241 TOCCATOCOGOTOACTOCCAAGAACCOGTGGAGCATGGATGACAACCTCATGCACATCAG 300 301 567 361 GÁCCCAGGACCCAGCCAAÁGCCCCCAÁCÁCCCCTGACÁTTCTCGAGÁTCGÁGTTCAÁÁAÁ 420 627 687 421 1047 gcaggtgtccgtcctcaagggccaggtgtacatcctcggccgggagtccccactgtctct 1106 541 481 747 1107 ctacaatgagga 1118 660 CAAACAAGGCCTGGGCTTGAAATTTGCTGAGCTGGTGTATACCGGTTTCTGGCACAG-CC 718 719 TGAGTGTGAATTTGTCCG-CACTGCATCGCCAAGTCCCCAGGAGCGAAGTGGAAGGAAAGT 777 778 GCAGGTGTCCGCCTCCA---GGCAGGTGTACATCCTCGGCGGATTCCCATGTCTCTCTCA 834 835 TGAGAGTGGTGA 846 attotacaaccggttcaagggccgcaatgacctgatggagtacgcaaagcaacacgggat 506 820; ctacgaggctggaatcctggagaaccccaagaaccaagcgcctccaggtctctacacgaa 626 CTACGAGGCTGGAATCCTGGAGAACCCCAAGAACCAAGCGCCTCCAGGTCTCTACACGAA 360 gacccaggacccagccaaagccccaacacccctgacattctcgagatcgagttcaaaaa 686 cctttaccatgctcatttagacatcgaggccttcaccatggaccgggaagtgcgcaaaat 926 GCTCTTCATGTACCTGAACGAAGTCGCGGGCAAGCATGGCGTGGGCCGTATTGACATCGT 540 gctcttcatgtacctgaacgaagtcgcggggcaagcatggcgtgggccgtattgacatcgt 806 h 61.2%; Similarity 96.2%; CCTTTACCATGCTCATTTAGACATCGAGG-CTTCACCATGGACCGGGAAGTGCGCAAAAT 659 caaacaaggcctgggcttgaaatttgctgagctggtgtataccggtttacggcctagccc 986 235 a Conservative California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)." a 275 c 266 g 176 t 0 Score 758.4; DB 10 pred. No. 7.7e-171; Mismatches DB 10; Indels Length 952; 6; Gaps

RESULT 10 BI085601

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SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
                            301 aaacaagtggaaatcgcccagcgggagggggccaagtatgtgtcccacggcgccacagga 360
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323 AAACAAGTGGAAATCGCCCAGGGGAGGGGGGCCAAAGTATGTGTCCCACGGCGCCACAGGA 382
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Tissue procurement: ATCC
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National Institutes of Health, Mammallan Gene Collection (MGC)
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/clone=lib="NIH_MGC_98"
/clone=lib="NIH_MGC_98"
/clone=lib="NIH_MGC_98"
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/note="organ: brain; Vector: point; Site_1: xhoI; Site_2:
/note="organ: brain; Vector: point; Site_1: xhoI; Site_2:
/tine EcoRI/XhoI sites using the following 5'
/cloned into EcoRI/XhoI
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                                                                                                                                                                                  cDNA Library Preparation: Ling Hong/Rubin Laboratory CNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov High quality sequence stop: 722.
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                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
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/Clone_lib="NIH_MGC_19"
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/tissue_type="neuroblastoma"
/lab_host="DH10B (phage-resistant)"
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                                                                                                            /clone="IMAGE:4098090"
                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
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871 GAACCACGAGGACCCCGGAGGACACCCT 898
                          839 gtatctacgagaccccagcaggcaccat 866
                                              813 AGCATGGAGTGGGCCGGAATGACATCGGGGAGAACCGCT--CATGGAATTGAAGCCCCCAG 870
                                                               779 agcatggcgtgggccgtattgacatcgtggagaaccgcttcattggaatgaagtcccgag 838
                                                                                                         753 TGGGACCAGCGAACAGAACCTCCTTGGAGCTCTCAAGGTACCTGAGCGAAAGTCCGGGCA 812
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                                                                                                                             720 tggcaccaccaccag-acctccttggagctcttcatgtacctgaacgaagtcgcgggca 778
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                                                                                                                                                                                    661 gacattotogagatogagattoaaaaaaggggtocotgtg-aaggtgaccaacgtoaagga 719
                                                                                                                                                                                                                                634 CAAGCGCCTCCAGGTCTCTACACGAAGACCCAGGACCCAAGGCCCAAAGCCCCCCAAGA-CCCT 692
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                                                                                                                                                                                                                                                                                                                                                                                                                                     421 gtcattgctccctggaggatgcctgaattctacaaccggttcaagggccgcaatgacctg 480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60.5%;
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Pred. No. 1.2e-168;
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BI253774
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 898)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NIH-MGC http://mgc.nci.nih.gov/
                                                                                                             DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM11280 row: 1 column: 06
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                         860;
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            GCACTGTATGAGGACCGCTACCTCCTGGGCACCTCTCTTGCCAGGCCCTGCATCGCCCGC 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: Incyte Genomics, Inc.
AAACAAGTGGAAATCGCCCAGCGGGAGGGGGCCAAGTATGTGTCCCACGGCGCCACAGGA
                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Organ: cervix: Vector: pcMV-spORT6; Site_1: Not1; Site_2: Sall: Cloned unidirectionally. Primer: Oligo dT Average insert size 1.4 kb. Library prepared by Life Technologies."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:9606"
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/clone_lib="NIH_MGC_12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
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/lab_host="DH10B"
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96.7%; Pred. No. 1.7e-168;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            660 tgacattctcgagatcgagttcaaaaaaggggtccctgtgaaggtgaccaacgtcaagga 719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   779 agcatggcgtgggccgtattgacatcgtggagaaccgcttcattggaatgaagtcccgag 838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       792 ACCATGGCGTGGGCCGTATGGACATCGTGGAGAAACGGTTCATTGGACTGAAGT-CCGAG 850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   851 GTATCTACGAGA-CCCAGGAGGCACATTCTTTACCATGCTCATTTAGA 898
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                                                                                        source
                                                                                                                                                                                                                                                                                                                                                                                                                                       BI258628 851 bp mRNA EST 1,70522004 502969566F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:5109064 5',
                                                                                                                                                                                                                                                                                                     Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 851)
                                                                                                                                                                                                                                                                                                                                                                                              BI258628.1 GI:14815170
                                                                                                                                                                                                                                                                                                                                                                                                                        mRNA sequence.
                                                                                                                                                                                                                                                                     Unpublished (1999)
                                                                                                                                                                                                                                                                                    NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                        cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                            Email: cgapbs-r@mail.nih.gov
                                                                                                                   High quality sequence stop: 849.
                                                                                                                                http://image.llnl.gov
plate: LLAM11264 row: c column: 17
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                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
/note="Organ: cervix; Vector: pCMV-SPORT6; Site_1: NotI;
                                                                                                          ocation/Qualifiers
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RESULT 14
                               836 TCTATTGAGACCC 848
                                                          841 atctacgagaccc 853
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                                                               778 CATGGCGTGGG-CGTATTGACATCGTGGAGAACCG-TTCATTGGAATGAAGTCCGAGGTA 835
                                                                               781 catggcgtgggccgtattgacatcgtggagaaccgcttcattggaatgaagtcccgaggt 840
                                                                                                                      720 G--ACCACCCACAGACCTCCTTGGAGCTCTTCATGTACCTGAACGAAAGTGGCGGGCAAG 777
                                                                                                                                   722 gcaccaccaccagacctcottggagctcttcatgtacctgaacg-aagtcgcgggcaag.780
                                                                                                                                                                            660 CATTCTCGAGATCGAGTTCAAAAAAAGGGGTCCTGTGAAGGTTGACCAACGTCAAGGATG 719
                                                                                                                                                                                              663 cattctcgagatcgagttcaaaaaaggggtccctgtgaagg-tgaccaacgtcaaggatg 721
                                                                                                                                                                                                                                    601 AGCGCCTCCAGGTCTCTACACGAAGACCCAGGACCCAGCCAAAGCCCCCAA-AACCCCTGA 659
                                                                                                                                                                                                                                                    603 agcgcctccaggtctctacacgaagacccaggacccagccaagcccccaacacccctga 662
                                                                                                                                                                                                                                                                                           541 GGATGAGAACCTCATGCACATCAGCTACGAGGCTGGAATCCTGGAGAACCCCAAGAACCA 600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  361 GGGGAACGATCAGGTCCGGTTTTGAGCTCAGCTGCTACTCACTGGCCCCCCAGATAAAGGT 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 ACTGTATGAGGACCGCTACCTCCTGGGCACCTCTCTTGCCAGGCCCTGCATCGCCGGCAA 300
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237 c 243 g 154 t
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AUTHORS
386 AAGGGGAACGATCAGGTCCGGTTTGAGCTCAGCTGCTACTCACTGGCCCCCCAGATAAAG
           361 aaggggaacgatcaggtccggtttgagctcagctgctactcactggccccccagataaag 420
                                                     326 AAACAAGTGGAAATCGCCCAGCGGGAGGGGGCCAAGTATGTGTCCCACGGCGCCACAGGA 385
                                                                      301 aaacaagtggaaatcgcccagcgggagggggccaagtatgtgtcccacggcgccacagga 360
                                                                                                               SOURCE
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                                                                                                                                                                                                                                                121 aaggaagacttcgaggaagccaggaagaaggcactgaagcttggggccaaaaaggtgttc 180
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                                                                                                                                                                                                                                                                                                         61 ctcgtgtggctgaaggaacaaggctatgacgtcattgcctatctggccaacattggccag 120
                                                                                                                                                                                                                                                                                                                                                  26 ATGTCCAGCAAAGGCTCCGTGGTTCTGGCCTACAGTGGCGGCCTGGACACCTCGTGCATC 85
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                                                                                                                                                                                                                                                                                                                                                                                                                                         829;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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Tissue procurement: ATCC

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Plate: LLAM11271 row: i column: 06 High quality sequence stop: 781.
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Plate: LLAM11271 row: i column: 06
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National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BI258439.1 GI:14814785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  602972421F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:5111885 5',
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note-"organ: cervix; Vector: pCMV-SPORT6; Site_1: Not1; Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT Average insert size 1.4 kb. Library prepared by Life 263 c 249 g 160 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="cervical carcinoma cell line"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="NIH_MGC_12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="IMAGE:5111885"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                            59.8%;
95.2%;
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 Mismatches

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ORGANISM

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DB 11; Length 851; Indels

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566 ATGGATGAGAACCTCATGCACATCAGCTACGAGGCTGGAAATCCTGGAGAACCCCCAAGAAC 625
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BI255104 851 bp mRNA EST 1/-JUL-2001 602975950F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:5115204 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 851)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mRNA sequence.
BI255104
                                                                                                                                                                                                                                                                                                                                                                                     Email: cgapbs-r@mail.nih.gov
Tissue procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               NIH MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1999)
                                                                                                                                                                                                                                                                found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                                                                                                                                                                                                                                                                                                    cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Incyte Genomics, Inc.
cDNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                              High quality sequence stop: 770.
                                                                                                                                                                                                                                                    Plate: LLAM11280
/note="Organ: cervix; Vector: pCMV-SPORT6; Site_1: Not1; Site_2: Sal1; Cloned unidirectionally. primer: Oligo dT syrage insert size 1.4 kb. Library prepared by Life Technologies."
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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GENERAL INFORMATION:
APPLICANT: Clark, Mike
APPLICANT: Holtsberg, Frederick Wayne
APPLICANT: Ensor Charles Mark
TITLE OF INVENTION: Methods For Predicting Su:
TITLE OF INVENTION: Therapy
FILE REFERENCE: PHOE-0060
CURRENT APPLICATION NUMBER: US/09/775,693
CURRENT FILLING DATE: 2001-02-02
UNBBER OF SEQ ID NOS: 10
SOFTWARE: Patentin version 3.0
LENGTH: 1239
TYPE: DNA
ORGANISM: Home serious
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           ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-577-410-7427
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; Sequence 7427, Application US/09577410
; GENERAL INFORMATION:
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SEQ ID NO 7427
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APPLICANT:
                                                                                                                   APPLICANT: MacKay, Charles
TITLE OF INVENTION: Nucleic Acid Molecules Derived from
TITLE OF INVENTION: Nucleic Acid Molecules Derived from
TITLE OF INVENTION: Human T Helper cell, Bone Marrow, and CD34+ Libraries
FILE REFERENCE: 5800-32
CURRENT APPLICATION NUMBER: US/09/577,410
CURRENT FILING DATE: 1000-05-23
PRIOR APPLICATION NUMBER: US 60/135,632
PRIOR FILING DATE: 1999-05-24
PRIOR APPLICATION NUMBER: US 60/135,633
PRIOR APPLICATION NUMBER: US 60/135,633
PRIOR APPLICATION NUMBER: US 60/135,616
PRIOR APPLICATION NUMBER: US 60/135,616
PRIOR FILING DATE: 1999-05-24
NUMBER: OF SEQ ID NOS: 8991
COUNTRIESE TEACTOR SERVICES
                                                                    LENGTH: . 1622
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APPLICANT: Williamson, Mark
APPLICANT: Shyjan, Andrew W.
APPLICANT: Shyjan, Andrew W.
TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
TITLE OF INVENTION: THEREFOR
FILLE REFERENCE: 1600.2021-001
CURRENT FILING NUMBER: US/09/338,425
CURRENT FILING DATE: 1999-06-22
PRIOR APPLICATION NUMBER: 60/168,038
PRIOR FILING DATE: 1999-11-30
PRIOR FILING DATE: 1999-11-30
NUMBER OF SEQ ID NOS: 2814
NUMBER OF SEQ ID NOS: 2814
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Pred. No. 6.1e-294;
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APPLICANT: Shyjan, Andrew W.
TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLE
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: 1600.1185-001
CUBRENT APPLICATION NUMBER: US/09/652,126
CURRENT FILING DATE: 2000-08-30
PRIOR APPLICATION NUMBER: 60/151,132
PRIOR FILING DATE: 1990-08-30
NUMBER OF SEQ ID NOS: 10051
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 9702
LENGTH: 1656
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ORGANISM: Homo sapiens
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99.7%; Pred. No. 6.1e-294;
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APPLICANT: Gutierrez-Ramos, Jose-Carlos
TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: 1600.1177-001
CURRENT FILING DATE: 2000-08-31
PRIOR APPLICATION NUMBER: 05/152,111
PRIOR APPLICATION NUMBER: 60/152,111
PRIOR APPLICATION NUMBER: 60/152,111
PRIOR FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 9647
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 9327
LENGTH: 1656
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; ORGANISM: HOMO
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Matches 1235; Conserv
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pred. No. 6.1e-294;
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RESULT 6
US-09-698-010-14283
; Sequence 14283, Application US/09698010
; GENERAL INFORMATION:
APPLICANT: Williamson, Mark
APPLICANT: Shyjan, Andrew W.
TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USTILE OF INVENTION: THEREFOR
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: 1600.2029-001
; CURRENT APPLICATION NUMBER: US/09/698,010
; CURRENT FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: 60/162,358
; PRIOR TILING DATE: 1999-10-29
; NUMBER OF SEQ ID NOS: 15684
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14283
; LENGTH: 1656
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; TYPE: DNA ; ORGANISM: Homo : US-09-698-010-14283

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CURRENT FILING DATE: 2000-10-27
PRIOR APPLICATION NUMBER: 60/162,166
PRIOR FILING DATE: 1999-10-28
NUMBER OF SEQ ID NOS: 9719
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TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: 1600.2002-001
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   APPLICANT: HUNTEY, John J.
APPLICANT: Shyjan, Andrew W.
APPLICANT: Stydan, Andrew TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND TITLE OF INVENTION: THEREFOR FILE REFERENCE: 1600.2036-001
CURRENT APPLICATION NUMBER: US/09/710,281
CURRENT FILING DATE: 2000-11-10
PRIOR APPLICATION NUMBER: 60/164,254
PRIOR FILING DATE: 1999-11-09
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SOFTWARE: FastSEQ
SEQ ID NO 5043
LENGTH: 1656
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FastSEQ for Windows Version
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GENERAL LIDYU, -- APPLICANT: LIDYU, -- APPLICANTION: NOVEL NUCLE.

TITLE OF INVENTION: THEREFOR

FILE REFERENCE: 1600 2041-001

CURRENT APPLICATION NUMBER: U3/09/716,920

CURRENT FILING DATE: 2000-11-20

PRIOR APPLICATION NUMBER: 60/166,507

PRIOR APPLICATION NUMBER: 1099-11-19

NUMBER OF SEQ ID NOS: 1641

SOFTWARE: FastSEQ for Windows Version 4.0
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US-09-716-920-1274
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SEQ ID NO 1274
LENGTH: 1656
TYPE: DNA
ORGANISM: Homo sapiens
US-09-716-920-1274
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                        aaacaagtggaaatcgcccagcgggaggggccaagtatgtgtcccacggcgcccacagga
      aaacaagtggaaatcgcccagcgggagggggccaagtatgtgtcccacggcgccacagga
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APPLICANT: Gearing, David P.
APPLICANT: Fraser, Christopher C.
APPLICANT: Donovan, Michael J.
APPLICANT: HOLTZMAN, Douglas A.
TITLE OF INVENTION: NOVEL NUCLEIC F
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: 1600.2054-001
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CURRENT FILING DATE: 2000-11-29
PRIOR APPLICATION NUMBER: 60/167,859
PRIOR EILING DATE: 1999-11-29
NUMBER OF SEQ ID NOS: 3770
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TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND TITLE OF INVENTION: THEREFOR FILE REFERENCE: 1600.2010-001

CURRENT APPLICATION NUMBER: US/09/726,787

CURRENT FILING DATE: 2000-11-30

PRIOR APPLICATION NUMBER: 60/168,132

PRIOR FILING DATE: 1999-11-30

NUMBER OF SEQ ID NOS: 3241

SOFTWARE: FastSEQ for window: "
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RESULT 12
US-09-726-790-2021
Sequence 2021, Application US/09726790; GENERAL INFORMATION:
APPLICANT: Williamson, Mark
APPLICANT: Shyjan, Andrew W.
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; ORGANISM: Homo
US-09-726-790-2021
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Best Local Similarity
Matches 1235; Conserv
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SEQ ID NO 2021
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CURRENT APPLICATION NUMBER: US/09/726,
CURRENT FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: 60/168,038
PRIOR FILING DATE: 1999-11-30
NUMBER OF SEQ ID NOS: 2814
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TITLE OF INVENTION:
FILE REFERENCE: 160
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                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 60/169,681
PRIOR FILING DATE: 1999-12-08
PRIOR FILING DATE: 1999-12-08
PRIOR FILING DATE: 1999-12-21
PRIOR APPLICATION NUMBER: US 60/171,350
PRIOR APPLICATION NUMBER: US 60/189,315
PRIOR APPLICATION NUMBER: US 60/203,791
PRIOR FILING DATE: 2000-05-12
PRIOR FILING DATE: 2000-05-12
PRIOR APPLICATION NUMBER: US 60/210,600
PRIOR FILING DATE: 2000-06-09
PRIOR FILING DATE: 2000-06-09
PRIOR FILING DATE: 2000-07-21
PRIOR FILING DATE: 2000-07-21
                                                   S.
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                                                                                                                                                      NUMBER OF SEQ ID NOS: 4660
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4186
                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Berger, Allison
APPLICANT: Zhao, Xumei
TITLE OF INVENTION: NOVEL GENES, COMPOSIT
TITLE OF INVENTION: METHODS FOR IDENTIFI
TITLE OF INVENTION: THERAPY OF CERVICAL
FILE REFERENCE: MRI-008B
                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Schlegal, Robert
APPLICANT: Deeds, James
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                       CURRENT FILING DATE: 2001-08-31
                                                   09-732-630-4186
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                                                                OTHER INFORMATION: n =
                                                                           NAME/KEY: misc_feature
LOCATION: 1,2,1725
                                                                                                                 ORGANISM: Homo sapiens
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                                                                                                                                           Q ID NO 4186
LENGTH: 1725
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99.7%;
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 Score 1232.6;
Pred. No. 6.16
    6.1e-294;
                DB 29; · Length 1725;
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                   841 atctacgagaccccagcaggcaccatcctttaccattgctcatttagacatcgaggccttc
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US-09-770-173-2339
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Matches 1235;
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TITLE OF INVENTION: MOVEL NUCLEIC ACID MOLECULES AND USES
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: 1600.2059-001
CURRENT APPLICATION NUMBER: US/09/770,173
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: US 60/178,876
PRIOR PILING DATE: 2000-01-28
NUMBER OF ESC. TO 2000-01-28
NUMBER OF ESC. TO 2000-01-28
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                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/760,475 CURRENT FILING DATE: 2001-01-16
                                                                                                                                                                                                                                          APPLICANT: Rosen et al. TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PTZ49
                                                                                                                                                         SOFTWARE: PatentIn Ver.
       OTHER INFORMATION: n equals a,t,g, or
                                                                   TYPE: DNA ORGANISM: Homo sapiens FEATURE:
NAME/KEY: SITE
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Copyright (c) 1993 - 2000 Compugen Ltd.
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US-09-998-598-702
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       Sequence 216, App Sequence 310, App Sequence 951, App Sequence 702, App Sequence 907, App Sequence 9145, App Sequence 9145, App Sequence 9145, App Sequence 914674, App Sequence 9166, App Sequence 1940, A Sequence 19540, A Sequence 19540, A Sequence 19540, A Sequence 19540, A Sequence 19772, Ap Sequence 2772, Ap Sequence 1772, Ap
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            APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL CONTIGS OBTAINED FROM VARIOUS CDNA
TITLE OF INVENTION: LIBRARIES
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PRIOR APPLICATION NUMBER: US/09/340,623
PRIOR FILING DATE: 1999-66-28
PRIOR APPLICATION NUMBER: US 09/205,070
PRIOR FILING DATE: 1998-12-03
NUMBER OF SEQ ID NOS: 45207
SOFTWARE: Fast-SEQ for Windows Version 3.0
SEQ ID NO 13594
LENGTH: 1828
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; OTHER INFORMATION: n = A,T,C
US-09-898-888A-13594
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                796
                                                                           658 cctgacattctcgagatcgagttcaaaaaaggggtccctgtgaaggtgaccaacgtcaag
                                                                                                                       676 aaccaagcgcctccaggtctctacacgaagacccaggacccagccaaagcccccaacacc
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              1 atgtccagcamaggctccgtggttctggcctacagtggcggcctggacacctcgtgcatc
gatggcaccacccaccagacctccttggagctcttcatgtacctgaacgaagtcgcgggc
                                                          cctgacattctcgagatcgagttcaaaaaaggggtccctgtgaaggtgaccaacgtcaag 795
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Pred. No. 0;
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CURRENT FILING DATE: 2001-12-12
PRIOR APPLICATION NUMBER: US 09/488,725
PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: US 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: PCT/US00/35017
PRIOR APPLICATION NUMBER: PCT/US00/35017
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 09/491,404
PRIOR APPLICATION NUMBER: US 09/491,404
PRIOR FILING DATE: 2000-10-25
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APPLICANT: Wang, Zhiwe
APPLICANT: Wang, Jian
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TITLE OF INVENTION: Novel Nucleic Acids and
TITLE OF INVENTION: Polypeptides
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                                                                                                                                   APPLICATION NUMBER: PCT/US01/03800 FILING DATE: 2001-02-05
                                                                                                                                                                            APPLICATION NUMBER: US 09/560,875 FILING DATE: 2000-04-27
                                                                                                                                                                                                                  APPLICATION NUMBER: US 09/496,914 FILING DATE: 2000-02-03
                                                                                                                                                                                                                                                         APPLICATION NUMBER: PCT, FILING DATE: 2001-01-25
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                                                       FILING DATE: 2000-02-28
APPLICATION NUMBER: US 09/577,409
FILING DATE: 2000-05-18
                                                                                                             APPLICATION NUMBER: US 09/515,126
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                 APPLICATION NUMBER: PCT/US01/04927 FILING DATE: 2001-02-26
APPLICATION NUMBER: US 09/519,705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wang, Zhiwei
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; LOCATION: (95)...(346)
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LENGTH: 2004
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PRIOR APPLICATION NUMBER: PCT/US01/14827
PRIOR FILING DATE: 2001-05-16
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PRIOR APPLICATION NUMBER: PCT/US01/08656
PRIOR FILING DATE: 2001-04-18
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PRIOR EILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: US 09/649,167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 1192
SOFTWARE: pt_FL_genes Version 6.0
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961 atggagtacgcaaagcaacacgggattcccatcccggtcactcccaagaacccgtggagc
                  481 atggagtacgcaaagcacacgggattcccatcccggtcactcccaagaacccgtggagc
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Pred. No. 0;
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GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Wang, Zihawel
APPLICANT: Wang, Jian-Ru
APPLICANT: Ghosh, Malabi
APPLICANT: Wang, Gezhi
APPLICANT: Weng, Gezhi
                                   PRIOR APPLICATION NUMBER: US 09/488,725
PRIOR FILING DATE: 2000-01-21
PRIOR FILING DATE: 2000-01-21
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: PCT/US00/35017
PRIOR APPLICATION NUMBER: PCT/US00/35017
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 09/491,404
PRIOR APPLICATION NUMBER: PCT/US01/02623
PRIOR APPLICATION NUMBER: PCT/US01/02623
PRIOR APPLICATION NUMBER: PCT/US01/02623
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APPLICANT:
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CURRENT ADDITION
                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/60/340,187 CURRENT FILING DATE: 2001-12-12
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FILING DATE: 2000-02-03
               APPLICATION NUMBER: US 09/496,914
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Ghosh, Malabika
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Boyle, Bryan J
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SEQ ID NO 330
LENGTH: 2005
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TYPE: DNA
ORGANISM: Homo :
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PRIOR FILING DATE: 2001-04-18
PRIOR APPLICATION NUMBER: US 09/577,408
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LOCATION: (254)..(2005)
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PRIOR FILING DATE: 2001-02-26
PRIOR APPLICATION NUMBER: US 09/519,705
PRIOR FILING DATE: 2000-03-07
PRIOR APPLICATION NUMBER: US 09/574,454
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PRIOR APPLICATION NUMBER: US 09/540,217
PRIOR FILING DATE: 2000-03-31
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PRIOR APPLICATION NUMBER: US 09/577,409
PRIOR FILING DATE: 2000-05-18
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361 aaggggaacgatcaggtccggtttgagctcagctgctactcactggccccccagataaag 420
                                       782 aaacaagtggaaatcgcccagcgggagggggccaagtatgtgtcccacggcgccacagga 841
                                                            301 aaacaagtggaaatcgcccagcgggagggggccaagtatgtgtcccacggcgccacagga 360
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FILING DATE: 2001-03-30
APPLICATION NUMBER: US 09/552,929
FILING DATE: 2000-04-18
                                                                                                                                            gcactgtatgaggaccgctacctcctgggcacctctctttgccaggccctgcatcgcccgc
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FILING DATE: 2000-08-23
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APPLICANT: Drmanac, Radoje T
TITLE OF INVENTION: Novel Nucleic Acids at
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 813
CURRENT APPLICATION NUMBER: US/60/340,187
CURRENT FILLING DATE: 2001-12-12
PRIOR APPLICATION NUMBER: US 09/488,725
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NAME/KBY: misc_feature
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TYPE: DNA
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APPLICATION NUMBER: US 09/577,409
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APPLICATION NUMBER: PCT/US01/08631
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APPLICATION NUMBER: PCT/US01/04927
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US-09-898-888A-22919

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Sequence 22919, Application GENERAL INFORMATION: APPLICANT: Hyseq, Inc.

US/09898888A

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; LOCATION: (1)...(987)
; OTHER INFORMATION: n =
US-09-898-888A-22919
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Best Local
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TITLE OF INVENTION: LIBRARIES
FILE REFERENCE: 20411-748CON1
CURRENT APPLICATION NUMBER: US/09/898,888A
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/340,623
PRIOR FILING DATE: 1999-06-28
PRIOR FILING DATE: 1999-06-28
PRIOR APPLICATION NUMBER: US/09/205,070
PRIOR FILING DATE: 1999-12-03
NUMBER OF SEQ ID NOS: 45207
SOFTWARE: FASTSEQ for Windows Version 3.0
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Pred. No. 2.6e-142;
0; Mismatches 4;
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RESULT 7
US-09-998-598-467/c
; Sequence 467, Application
; GENERAL INFORMATION:
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CURRENT FILING DATE: 2001-11-16
NUMBER OF SEQ ID NOS: 2606
SOFTWARE: Corixa Invention Disclosure Database
SEQ ID NO 467
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Best Local Similarity
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APPLICANT: Meagher, Madelein Joy
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER
FILE REFERENCE: 210121.561
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                              agg 935
                                                             CCATGCTCATTTAGACATCGAGGCCTTCACCATGGACCGGGAAGTGCGCAAAATCAAACA 4
                                                                                                                             CCGCTTCATTGGAATGAAGTCCCGAGGTATCTACGAGACCCCAGCAGGCACCATCCTTTA 64
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                                                                              ccatgctcatttagacatcgaggccttcaccatggaccgggaagtgcgcaaaatcaaaca 932
                                                                                                                                                                                              CATGTACCTGAACGAAGTCGCGGGCAAGCATGGCGTGGGCCGTATTGACATCGTGGAGAA 124
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; TYPE: DNA; Homo sapiens; ORGANISM: Homo sapiens US-09-998-598-702
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CURRENT FILING DATE: 2001-11-16
NUMBER OF SEQ ID NOS: 2606
SOFTWARE: COTIXA Invention Disclosure Database
SEQ ID NO 702
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APPLICANT: Xu, Jiangchun
APPLICANT: Chenault, Ruth A.
APPLICANT: Meagher, Madelein Joy
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 503;
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Best Local
                                                                                                                       Sequence 907, Application US/09998598 GENERAL INFORMATION:
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APPLICANT: Stolk, John A.
APPLICANT: Xu, Jiangchun
APPLICANT: Chenault, Ruth A.
APPLICANT: Meagher, Madelein Joy
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER
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Similarity 100.0%; Pred. No. 3.2e-128;
O: Mismatches 0;
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; ORGANISM: Homo sapiens US-09-998-598-924
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-998-598-907
                                                           NUMBER OF SEQ ID NOS: 2606
SOFTWARE: Corixa Invention Disclosure Database
SEQ ID NO 924
                                                                                                                                                                                                                                                                            Sequence 924, Application US/09998598 GENERAL INFORMATION:
                                                                                                                CURRENT APPLICATION NUMBER: US/09/998,598
CURRENT FILING DATE: 2001-11-16
                                                                                                                                                       APPLICANT: Stolk, John A.
APPLICANT: Xu, Jiangchun
APPLICANT: Xu, Jiangchun
APPLICANT: Chenault, Ruth A.
APPLICANT: Meagher, Madelein Joy
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER
ETILE REFERENCE: 210121.561
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Best Local Similarity 100.0%; Pred. No. 3.2e-128;
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                                   TYPE: DNA
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CURRENT APPLICATION NUMBER: US/09/998,598
CURRENT FILING DATE: 2001-11-16
NUMBER OF SEQ ID NOS: 2606
SOFTWARE: Corixa Invention Disclosure Database
                                                   LENGTH: 503
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; ORGANISM: Homo sapiens
US-09-998-598-1365
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; GENERAL INFORMATION:
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                                                                                                                                                                                                                           SOFTWARE: Corixa Invention Disclosure Database
SEQ ID NO 1365
LENGTH: 503
                                                                                   Matches 501;
                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                APPLICANT: Stolk, John A.
APPLICANT: Xu, Jiangchun
APPLICANT: Chenault, Ruth A.
APPLICANT: Chenault, Ruth A.
APPLICANT: Meagher, Madelein Joy
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER
FILE REFERENCE: 210121.561
CURRENT APPLICATION NUMBER: US/09/998,598
CURRENT APPLICATION NUMBER: US/09/998,598
RUMBER OF SEQ ID NOS: 2606
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Best Local Similarity
                 393 otgotactcactggccccccagataaaggtcattgctccctggaggatgcctgaattcta 452
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CTGCTACTCACTGGCCCCCCAGATAAAGGTCATTGCTCTCTGGAGGATGCCTGAATTCTA 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99acccagccaaagcccccaacacccctgacattctcgagatcgagttcaaaaaaggggt 692
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100.0%; Pred. No. 3.2e-128;
tive 0; Mismatches 0;
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                                                                           Score 499.8; DB 7;
Pred. No. 2.4e-127;
0; Mismatches 2;
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; GENERAL INFORMATION:
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CURRENT FILING DATE: 2001-11-16
NUMBER OF SEQ ID NOS: 2606
SOFTWARE: Corixa Invention Disclosure Database
SEQ ID NO 787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Stolk, John A.
APPLICANT: Xu, Jiangchun
APPLICANT: Chenault, Ruth A.
APPLICANT: Meagher, Madelein Joy
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER
FILE REFERENCE: 210121.561
                                                                                                                                                                                                                                                                                    Matches 468; Conservative
                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 469
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                                                                                                                                                                                                                              427 gctccctggaggatgcctgaattctacaaccggttcaagggccgcaatgacctgatggag 486
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                                                                                                                                                                                                          1 gctccctggaggatgcctgaattctacaaccggttcaagggccgcaatgacctgatggag 60
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cctccaggtctctacacgaagacccaggacccaggccaaagcccccaacacccctgacatt 666
                                                        gagaacctcatgcacatcagctacgaggctggaatcctggagaaccccaagaaccaagcg 180
                                                                          gagaacctcatgcacatcagctacgaggctggaatcctggagaaccccaagaaccaagcg 606
                                                                                                                                tacgcaaagcaacacgggattccccatcccggtcactcccaagaacccgtggagcatggat 120
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                                                                                                                                                                                                                                                                                                        37.7%; Score 467.4; DB 7; Length 469; 99.8%; Pred. No. 1.9e-118;
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PRIOR FILING DATE: 2000-05-17
PRIOR FILING DATE: 2000-05-17
NUMBER OF SEQ ID NOS: 116231
SOFTWARE: Hy-patent.pl Version 3.1
SEQ ID NO 54674
LENGTH: 479
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Novel Nucleic Acid Sequences Obtained TITLE OF INVENTION: From Various Libraries
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                         123
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                                                                                                      243 actgtatgaggaccgctacctcctgggcacctctcttgccaggccctgcatcgcccgcaa
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                                                                                                                                                                                                                          cgtgtggctgaaggaacaaggctatgacgtcgttgcctatctggccaacattggccagaa
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ggggaacgatcaggtccggtttgagctcagctgctactcactggccccccagataaaggt 422
                                                                                                                                                                                                                                                                                                                                                                                                          h 36.9%; Score 457.4; DB 6; Similarity 99.8%; Pred. No. 1.1e-115;
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Stache-Crain, Birgit
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LENGTH: 538
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APPLICANT: Rank, David R.
APPLICANT: Hanzel, David R.
APPLICANT: HAZEL, DAVID K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
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OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.76

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.7

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.4

OTHER INFORMATION: NT HIT: 9114740527, EVALUE 0.00e+00

OTHER INFORMATION: SMISSPROT HIT: P00966, EVALUE 3.00e-74

OTHER INFORMATION: EST_HUMAN HIT: BE783168.1, EVALUE 0.00e+00
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CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 34288 SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
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                      523 cccaagaacccgtggagcatggatgagaacctcatgcacatcagctacgaggctggaatc 582
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                                                                                                                                                                                                                                                                                                                            284 ggccctgcatcgcccgcaaacaagtggaaatcgcccagcgggaggggggccaagtatgtgt 343
                                                                                                                                                                                                                                                                                                                                                                                   418 TGGCCATCCAGTCCAGCGCACTGTATGAGGACCACTACCTCCTGGGCCACCTCTCTCACCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                             478 GGGGCAAAAAGGTGTTCATTGAGGAAGTCAGCAAGGAGTTTGTGAAGGAGTTCATCTGGC 419
                                                                                                                                                                                                                                                                                                                                                                                                        224 cggccatccagtccagcgcactgtatgaggaccgctacctcctggggcacctctcttgcca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    164 999ccaaaaaggtgttcattgaggatgtcagcagggagtttgtgggggggttcatctggc 223
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CCCAAGAACCTGTGGAACATGGACGAGAACCTCATGCAGATCAGCAATGAGGCTGGAATC
                                                                                              aagggccgcaatgacctgatggagtacgcaaagcaacacgggattcccatcccgggtcact 522
                                                                           AAGGTCCGAAATGACCTTATGGAACACACAAAGCAACACGGGATTCCCCATCCCAGTCACT 119
                                                                                                                                                   TGCCCCCCAGATAAAGGTCATTGCTCCCTGGAGGATGCCCAAGTTCTACAACAGGTTC 179
                                                                                                                                                                          t99-cccccagataaaggtcattgctccctggaggatgcctgaattctacaaccggttc 462
                                                                                                                                                                                                                                                        | CCCacggcgccacaggaaaggggaacgatcaggtccggtttgagctcagctgctactcac 403
                                                                                                                                                                                                                               CCCACAGCGCCACAGGAAAGGGAAATGATCAGGTCCAGTTTGAGCTAAACTGCTACTCTC
                                                                                                                                                                                                                                                                                                         TGGCCAACACTGGCCAGAAGGAAGACTTTGAGGAAGCCAGGAAGAAGGCACTGAAGCTTG 479
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91.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 266, Application US/09922340 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 266,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 1999-07-14
PRIOR APPLICATION NUMBER: US 09/004,182
PRIOR FILING DATE: 1998-01-07
NUMBER OF SEQ ID NOS: 12181
SOFTMARE: FASTSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT FILING DATE: 2001-08-03
PRIOR APPLICATION NUMBER: 09/353,690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/922,340 CURRENT FILING DATE: 2001-08-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Novel Nucleic Acid Sequences Obtained TITLE OF INVENTION: From cDNA Libraries Of Fetal Liver-Spleen and Infant Brain FILE REFERENCE: 20411-726CON2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(465)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Hyseq,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
                  754 atgtacctgaacgaagtcgcgggcaagcatggcgtgggc 792
                                                                361 cctgtgaaggtgaccaacgtcaaggatggtaccaccnaccagacctccttggagctcttc
                                                                                   634 gacccagccaaagcccccaacacccctgacattctcgagattcgagattcaaaaaaggggtc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 465
                                                                                                                                                                                                        241 gctggaatcctggagaaccccaagaaccaagcgcctccaggtctctacacgaagacccag
                                                                                                                                                                                                                                                                                             181
                                                                                                                                                                                                                                                                                                                                                                     454 aaccggttcaagggccgcaatgacctgatggagtacgcaaagcaacacgggattcccatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               334 aagtatgtgtcccacggcgccacaggaaaggggaacgatcaggtccggtttgagctcagc
                                                                                                                                                                                                                                                                                                                                                                                                                                         394 tgctactcactggcccccagataaaggtcattgctccctggaggatgcctggattctac 453
                                                                                                                                                                                                                                                                                                                                                                                                                      61 tgctactcactggccccccagataaaggtcattgctccctggaggatgcctgaattctac
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atgtacctgaacgaagtcgcgggcaagcatggcgtggcc 459
                                                                                                                                      gacccagccaaagcccccaacacccctgacattctcgagatcgagttcaaaaaaggggtc
                                                                                                                                                                                                                             gctggaatcctggagaaccccaagaaccaagcgcctccaggtctctacacgaagacccag 633
                                                                                                                                                                                                                                                                                                                                                aaccggttcaagggccgcaatgacctgatggagtacgcaaagcaacatgggattcccatc 180
                                                                                                                                                                                                                                                                            ccggtcactcccaagaacccgtggagcatggatgagaacctcatgcacatcagctacgag
                                                                                                                                                                                                                                                                                                 | CC99tCactcccaagaacccgtggagcatggatgagaacctcatgcacatcagctacgag 573
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99.1%;
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Pred. No. 1.5e-114;
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OM of: US-09-775-693-1 to: Pending_Patents_AA_Main: * out_format : pfs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            About: Results were produced by the GenCore software, version 4 Copyright (c) 1993-2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Date: Feb 12, 2002 4:00 PM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Command line parameters:
                                                                                                                                                                                                                                                                                                                           Database: Pending_Patents_AA_Main:*
Database sequences: 3148936
Database length: 277657034
                                                                                                                                                                                                                                                                                                                                               Query length: 1239
                                                                                                                                                                                                                                                                                                                                                       Search information block: Query: US-09-775-693-1
                                                                                                                                                                                                                                                                                                                      Search time (sec): 324.520000
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                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
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/cgn2_6/ptodata/2/paa/US60_COMB.pep:US-09-401-151-18 + 895.00 1265.86 1.8e-62 /cgn2_6/ptodata/2/paa/US60_COMB.pep:US-60-312-544-5456 + 894.50 1262.41 2.1e-62 /cgn2_6/ptodata/2/paa/US60_COMB.pep:US-60-324-109-21424 + 894.50 1262.41 2.1e-62 /cgn2_6/ptodata/2/paa/US60_COMB.pep:US-60-186-280-522 + 888.00 1261.26 5.4e-62 /cgn2_6/ptodata/2/paa/US60_COMB.pep:US-60-195-311-672 + 881.50 1252.09 1.8e-61 /cgn2_6/ptodata/2/paa/US60_COMB.pep:US-60-195-311-672 + 881.50 1252.09 1.8e-61
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PRIOR FILING DATE: 1999-04-01
PRIOR APPLICATION NUMBER: 60/178,965
PRIOR FILING DATE: 2000-02-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Giot, Loic A. APPLICANT: Mansfield, Traci A. TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same FILE REFERENCE: 15966-542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/538,092
CURRENT FILING DATE: 2000-03-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 101 ATCTGGCCAACATTGGCCAGAAGGAAGACTTCGAGGAAGCCAGGAAGAAG
                                                                                                                                                                                                                                                                                                 151 GCACTGAAGCTTGGGGCCAAAAAAGGTGTTCATTGAGGATGTCAGCAGGGA 200
351 CGCCACAGGAAAGGGGAACGATCAGGTCCGGTTTGAGCTCAGCTGCTACT 400
                                               251 AGGACCGCTACCTCCTGGGCACCTCTCTTGCCAGGCCCTGCATCGCCCGC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51 CTCGTGCATCCTCGTGTGGCTGAAGGAACAAGGCTATGACGTCATTGCCT 100
                                                                                                                                                                                                                                                 67 uPheValGluGluPheIleTrpProAlaIleGlnSerSerAlaLeuTyrG
                                                                                                                                                                                                                                                                                                                                                 51 AlaLeuLysLeuGlyAlaLysLysValPheIleGluAspValSerArgGl 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                   34 yrLeuAlaAsnIleGlyGlnLysGluAspPheGluGluAlaArgLysLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ATGTCCAGCAAAGGCTCCGTGGTTCTGGCCTACAGTGGCGGCCTGGACAC
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                                                                                                  AAACAAGTGGAAATCGCCCAGCGGGAGGGGGCCCAAGTATGTGTCCCACGG
                                                                                                                                               luAspArgTyrLeuLeuGlyThrSerLeuAlaArgProCysIleAlaArg 100
                                                                                                                                                                                                                                                                       Quality: 2144.00
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1151 AGCCAACTGATGCCACCGGGTTCATCAACATCAATTCCCTCAGGCTGAAG 1200
                1201 GAATATCATCGTCTCCAGAGGAAGGTCACTGCCAAA 1236
                                                                                                                                      1101 GTCTCTCTACAATGAGGAGCTGGTGAGCATGAACGTGGAGGGTGATTATG 1150
                                                                                                                                                                                                  1051 GTGTCCGTCCTCAAGGGCCAGGTGTACATCCTCGGCCGGGAGTCCCCACT 1100
                                                                                                                                                                                                                                                               1001 TCCGCCACTGCATCGCCAAGTCCCAGGAGGGAAGGGGAAAGGGAAAGTGCAG 1050
401 GluTyrHisArgLeuGlnSerLysValThrAlaLys 412
                                                          367 uSerLeuTyrAsnGluGluLeuValSerMetAsnValGlnGlyAspTyrG 384
                                                                                                                                                                                   351 ValSerValLeuLysGlyGlnValTyrIleLeuGlyArgGluSerProLe 367
                                                                                                                                                                                                                                               334 alargHisCysIleAlaLysSerGlnGluArgValGluGlyLysValGln 350
                                                                                                                                                                                                                                                                                                           317 eAlaGiuLeuValTyrThrGlyLeuArgProSerProGluCysGluPheV 334
                                                                                                                                                                                                                                                                                                                                                                      951 TGCTGAGCTGGTGTATACCGGTTTACGGCCTAGCCCTGAGTGTGAATTTG 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                 851 CCCCAGCAGCACCATCCTTTACCATGCTCATTTAGACATCGAGGCCTTC 900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                267 plievalGluAsnArgPheIleGlyMetLysSerArgGlyIleTyrGluT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            801 CATCGTGGAGAACCGCTTCATTGGAATGAAGTCCCGAGGTATCTACGAGA 850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          751 TTCATGTACCTGAACGAAGTCGCGGGCAAGCATGGCGTGGGCCGTATTGA 800
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          167 sGlyIleProIleProValThrProLysAsnProTrpSerMetAspGluA 184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    451 TACAACCGGTTCAAGGGCCGCAATGACCTGATGGAGTACGCAAAGCAACA 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  401 CACTGGCCCCCAGATAAAGGTCATTGCTCCCTGGAGGATGCCTGAATTC 450
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seq_name: /cgn2_6/ptodata/2/paa/US097_COMB.pep:US-09-775-693-7
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alignment_block:
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//sequence 7, Applification US/09778693.
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APPLICANT: Clark, Mike
501 CGGGATTCCCATCCCGGTCACTCCCAAGAACCCGTGGAGCATGGATGAGA 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Holtsberg, Frederick Wayne
APPLICANT: Ensor, Charles Mark
TITLE OF INVENTION: Methods For Predicting Susceptibility Of Patients To Arginine
FILE REFERENCE: PHOE-0060
                                                                        151 TyrasnargPheLysGlyargAsnaspLeuMetGluTyralaLysGlnHi 167
                                                                                                                                              134 erLeuAlaProGlnIleLysValIleAlaProTrpArgMetProGluPhe 150
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CURRENT FILING DATE: 2001-02-02
NUMBER OF SEQ ID NOS: 10
                                                                                           451 TACAACCGGTTCAAGGGCCGCAATGACCTGATGGAGTACGCAAAGCAACA 500
                                                                                                                                                                   401 CACTGGCCCCCAGATAAAGGTCATTGCTCCCTGGAGGATGCCTGAATTC 450
                                                                                                                                                                                                                        351 CGCCACAGGAAAGGGGAACGATCAGGTCCGGTTTGAGCTCAGCTGCTACT 400
                                                                                                                                                                                                                                                                                              101 LysGinvalGluIleAlaGlnArgGluGlyAlaLysTyrValSerHisGl 117
                                                                                                                                                                                                                                                                                                                                 301 AAACAAGTGGAAATCGCCCAGCGGGAGGGGGGCCAAGTATGTGTCCCACGG 350
                                                                                                                                                                                                                                                                                                                                                                  151 GCACTGAAGCTTGGGGCCCAAAAAGGTGTTCATTGAGGATGTCAGCAGGGA 200
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Ratio: 5.204
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Sequence 87, Application US/60239841
GENERAL INFORMATION:
APPLICANT: LASEK, AMY W.
APPLICANT: JONES, DAVÍG A.
TITLE OF INVENTION: GENES EXPRESSED IN COLK
FILE REFERENCE: PA-0038 P
CURRENT APPLICATION NUMBER: US/60/239,841
CURRENT FILING DATE: 2000-10-11
NUMBER OF SEQ ID NOS: 194
SOFTWARE: PERL Program
SEQ ID NO 87
                                                                                                                                                                                                                                                              seq_documentation_block:
                                                                                                                                                                                                                                                                                                     seq_name: /cgn2_6/ptodata/2/paa/US60_COMB.pep:US-60-239-841-87
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LENGTH: 412
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                                                                                                                                                                                                                                                                                                                                              GluTyrHisArgLeuGlnSerLysValThrAlaLys 412
                                                                                                                                                                                                                                                                                                                                                                                                                                       luProThrAspAlaThrGlyPheIleAsnIleAsnSerLeuArgLeuLys
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alignment_scores:
Quality: 2123.00
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US-09-775-693-1 x US-60-239-841-87
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Percent Similarity:
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151
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                                                                GlnAlaProProGlyLeuTyrThrLysThrGlnAspProAlaLysAlaPr
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seq_documentation_block:
    Sequence 1594, Applicati
    GENERAL INFORMATION:
    APPLICANT: Craig Rosen,
    APPLICANT: Steve Ruben
    TITLE OF INVENTION: Hum
    FILE REFERENCE: PA101PC
    CURRENT APPLICATION NUM
    CURRENT EPPLICATION NUM
    CURRENT EPPLICATION NUM
    CURRENT FILING DATE: 20
    EARLIER APPLICATION NUM
    EARLIER FILING DATE: 10

                                                                                                                                                                                                                                                                APPLICANT: Craig Rosen,
APPLICANT: Steve Ruben
TITLE OF INVENTION: Human Prostate Cancer Associated Gen
FILE REFERENCE: PA101PCT
CURRENT APPLICATION NUMBER: PCT/US00/05988
CURRENT FILING DATE: 2000-03-08
EARLIER APPLICATION NUMBER: 60/124,270
EARLIER FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1890
SOFTWARE: Patentin Ver. 2.0
                                                                                               ; LOCATION: (22)
; OTHER INFORMATION:
PCT-US00-05988-1594
                                       alignment_scores:
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                                                                                                                                                                                                                                                      SEQ ID NO 1594
                                                                                                                                                                                                               LENGTH: 442
TYPE: PRT
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 Quality:
Ratio:
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                                                                                                               L-amino
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Align seg 1/1
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 801
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                                                                                                  AGGTGACCAACGTCAAGGATGGCACCACCACCAGCCTCCTTGGAGCTC
                                                                                                                                             oAsnThrProAspIleLeuGluIleGluPheLysLysGlyValProValL
                                                                                                                                                                                                                                                                                                                                                                                                             TACAACCGGTTCAAGGGCCGCAATGACCTGATGGAGTACGCAAAGCAACA
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                                                                                   ysValThrAsnValLysAspGlyThrThrHisGlnThrSerLeuGluLeu
                                                                                                                                                                                                                                                               snLeuMetHisTleSerTyrGluAlaGlyIleLeuGluAsnProLysAsn
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CURRENT APPLICATION NUMBER: PCT/US00/26524B
CURRENT FILING DATE: 2000-09-28
CURRENT FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: 60/157,137
PRIOR FILING DATE: 1999-09-29
PRIOR APPLICATION NUMBER: 60/163,280
PRIOR FILING DATE: 1999-11-03
NUMBER OF SQL ID NOS: 8564
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 6180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: (22)
COTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids pcT-US00-26524B-6180
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APPLICANT: Birse et. al.
TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
TITLE OF INVENTION: COLOR OF THE PROPERTY 
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Ratio: 5.178
Percent Similarity: 99.515
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                                                                                                               Align seg 1/1 to: PCT-US00-26524B-6180 from: 1 to: 442
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
NAME/KEY: SITE
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1 ATGTCCAGCAAAGGCTCCGTGGTTCTGGCCTACAGTGGCGGCCTGGACAC 50
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101 ATCTGGCCAACATTGGCCAGAAGGAAGACTTCGAGGAAGCCAGGAAGAAG 150
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                                                                                                                                                                                                                                                                                                                                                                                                   501 CGGGATTCCCCATCCCGGTCACTCCCAAGAACCCGTGGAGCATGGATGAGA 550
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                                                                                                                                                                                                                                    651 CAACACCCCTGACATTCTCGAGATCGAGTTCAAAAAAGGGGGTCCCTGTGA 700
                                                                                                                                                                                    701 AGGTGACCAACGTCAAGGATGGCACCACCACCAGACCTCCTTGGAGCTC 750
                                                                                           751 TTCATGTACCTGAACGAAGTCGCGGGCAAGCATGGCGTGGGCCGTATTGA 800
                                                                                                                                         281 PheMetTyrLeuAsnGluVaiAlaGlyLysHisGlyValGlyArglieAs 297
                                              314 hrProAlaGlyThrileLeuTyrHisAlaHisLeuAspIleGluAlaPhe 330
                                                                      851 CCCCAGCAGCACCATCCTTTACCATGCTCATTTAGACATCGAGGCCTTC 900
                     901 ACCATGGACCGGGAAGTGCGCAAAATCAAACAAGGCCTGGGGCTTGAAATT 950
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alignment_block:
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CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05988
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1594
                                                                                                                                                                                                                                                                                                                                                        ; NAME/KEY: SITE
; LOCATION: (22)
; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
US-09-925-300-1594
                                                                                                                                                                              Align seg 1/1 to: US-09-925-300-1594 from: 1 to: 442
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Ratio: 5.178 Gaps: 0
Percent Similarity: 99.515 Percent Identity: 99.272
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              101 ATCTGGCCAACATTGGCCAGAAGGAAGACTTCGAGGAAGCCAGGAAGAAG 150
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ORGANISM: Homo sapiens
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                                          47 rSerCysileLeuValTrpLeuLysGluGinGlyTyrAspValIleAlaT 64
                                                                           51 CTCGTGCATCCTCGTGTGGCTGAAGGAACAAGGCTATGACGTCATTGCCT 100
                                                                                                         1151 AGCCAACTGATGCCACCGGGTTCATCAACATCAATTCCCTCAGGCTGAAG 1200
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364 alargHisCysTleAlaLysSerGlnGluargValGluGlyLysValGln 380
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364 alArgHisCysTleAlaLysSerGlnGluArgValGluGlyLysValGln 380
                                                        347 eAlaGluLeuValTyrThrGlyPheTrpHisSerProGluCysGluPheV 364
                                                                          951 TGCTGAGCTGGTGTATACCGGGTTTACGGCCTAGCCCTGAGTGTGAATTTG 1000
                                                                                                                331 ThrMetAspArgGluValArgLysIleLysGinGlyLeuGlyLeuLysPh 347
                                                                                                                                901 ACCATGGACCGGGAAGTGCGCAAAATCAAACAAGGCCTGGGCTTGAAATT 950
                                                                                                                                                                          314 hrProAlaGlyThrIleLeuTyrHisAlaHisLeuAspIleGluAlaPhe 330
                                                                                                                                                                                                     851 CCCCAGCAGGCACCATCCTTTACCATGCTCATTTAGACATCGAGGCCTTC 900
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                                                                                                                                                                                                                                                                                                           751 TTCATGTACCTGAACGAAGTCGCGGGCAAGCATGGCGTTGGGCCGTATTGA 800
                                                                                                                                                                                                                                                                                            281 PheMetTyrLeuAsnGluValAlaGlyLysHisGlyValGlyArgIleAs 297
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seq_name: /cgn2_6/ptodata/2/paa/US097_COMB.pep:US-09-760-475-2729
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NAME/KEY: SITE
LOCATION: (14)
OTHER INFORMATION: Xaa equals any of the naturally occurring
NAME/KEY: SITE
LOCATION: (17)
OTHER INFORMATION: Xaa equals any of the naturally occurring
US-09-760-475-2729
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Ratio: 5.178
Percent Similarity: 99.515
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GENERAL INFORMATION:
APPLICANT: Rosen et al.
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LENGTH: 473
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CURRENT APPLICATION NUMBER: US/09/760,475
CURRENT FILING DATE: 2001-01-16
Prior application data removed - consult PALM or file wrapponumber of SEQ ID NOS: 4122
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                                                                                                                                                                                                                                                          51 CTCGTGCATCCTCGTGTGGCTGAAGGAACAAGGCTATGACGTCATTGCCT 100
                                                                                                                                                                                                                                                                                                                        62 MetSerSerLysGlySerValValLeuAlaTyrSerGlyGlyLeuAspTh 78
                                                                                                                                                                                                                                                                                                                                                                1 ATGTCCAGCAAAGGCTCCGTGGTTCTGGCCTACAGTGGCGGCCTGGACAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             uSerLeuTyrAsnGluGluLeuValSerMetAsnValGlnGlyAspTyrG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTCTCTCTACAATGAGGAGCTGGTGAGCATGAACGTGCAGGGTGATTATG 1150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCACTGAAGCTTGGGGCCAAAAAGGTGTTCATTGAGGATGTCAGCAGGGA
rSerCysIleLeuValTrpLeuLysGluGlnGlyTyrAspValIleAlaT
                                                                              AlaLeuLysLeuGlyAlaLysLysValPheIleGluAspValSerArgGl
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178 yAlaThrGlyLysGlyAsnAspGlnValArgPheGluLeuSerCysTyrS
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          1101 GTCTCTACAATGAGGAGCTGGTGAACCATGAACGTGCAGGGTGATTATG 1150
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                                                                                                                                                                                                                                                                                                                                           551 ACCTCATGCACATCAGCTACGAGGCTGGAATCCTGGAGAACCCCCAAGAAC
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                                                                 1051 GTGTCCGTCCTCAAGGGCCAGGTGTACATCCTCGGCCGGGAGTCCCCACT 1100
                                                                                                                                                                                                                       951 TGCTGAGCTGGTGTATACCGGTTTACGGCCCTAGCCCTGAGTGTGAATTTG 1000
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                                                                                                                                                                                                                                                                                                           901 ACCATGGACCGGGAAGTGCGCAAAATCAAACAAGGCCTGGGCTTGAAATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 801 CATCGTGGAGAACCGCTTCATTGGAATGAAGTCCCGAGGTATCTACGAGA
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428 uSerLeuTyrAsnGluGluLeuValSerMetAsnValGlnGlyAspTyrG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TyrAsnArgPheLysGlyArgAsnAspLeuMetGluTyrAlaLysGlnHi
                                                                                                                                  alArgHisCysIleAlaLysSerGlnGluArgValGluGlyLysValGln 411
                                                                                                                                                                                                                                                                        TCCGCCACTGCATCGCCAAGTCCCAGGAGCGAGTGGAAGGGGAAAGTGCAG 1050
                                                                                                                                                                                                       eAlaGluLeuValTyrThrGlyPheTrpHisSerProGluCysGluPheV
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alignment_block:
US-09-775-693-1 x US-60-207-216-791
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: F
SEQ ID NO 791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Beasley, Ellen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 791, Application US/60207216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: ISOLATED HUMAN DRUG TARGET PROTEINS,
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CL000580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/60/207,216
CURRENT FILING DATE: 2000-05-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 425
TYPE: PRT
                                                                                                                       351 CGCCACAGGAAAGGGGAACGATCAGGTCCGGTTTGAGCTCAGCTGCTACT 400
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                                                                                                                                                                                                                                                                                                                                                                           100 AlaProLysLeuGlyThrLysLysValPheThrGluGlyValSerArgGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                             151 GCACTGAAGCTTGGGGCCCAAAAAGGTGTTCATTGAGGATGTCAGCAGGGA 200
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                                                                                                                                                                                                                                                   luAspGlyTyrLeuLeuGlyThrSerHisThrArgProCysThrAlaArg 149
                                                                                                                                                                                                            AAACAAGTGGAAATCGCCCAGCGGGAGGGGGCCAAGTATGTGTCCCACGG 350
                                                                                                                                                                                                                                                                                                                                      uPheValGluGluPheIleTrpProAlaIleGlnSerSerSerLeuTyrG 133
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Ratio: 4.660
milarity: 84.951
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seq_documentation_block:
    Sequence 34811, Application PC/TUS0108631
    GENERAL INFORMATION:
    APPLICANT: Hyseq, Inc
    TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
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seq_name: /cgn2_6/ptodata/2/paa/PCTUS_COMB.pep:PCT-US01-08631-34811
                                                                                                                                                                                              1150 GAGCCAACTGATGCCACCGGGTTCATCAACATCAATTCCCCTCAGGCTGAA 1199
                                                                                                                                                                                                                                                                                                  1100 TGTCTCTACAATGAGGAGCTGGTGAGCATGAACGTGCAGGGTGATTAT 1149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1000 GTCCGCCACTGCATCGCCAAGTCCCAGGAGCGAGTGGAAGGGGAAAGTGCA 1049
                                                                                                    1200 GGAATATCATCGTCTCCAGAGCAAGGTCACTGCC 1233
                                                                                                                                                                                                                                                                                                                                                                                                    1050 GGTGTCCGTCCTCAAGGGCCAGGTGTACATCCTCGGCCGGGAGTCCCCAC 1099
                                                  413 sGluTyrHisHisLeuGlnSerLysValThrAla 424
                                                                                                                                                                                                                                             380 rgSerLeuTyrAsnGluGluLeuValSerMetAsnValHisGlyAspTyr 396
                                                                                                                                                                                                                                                                                                                                               363 nValSerLeuPheLysAspGlnValTyrIleLeuGlyTrpGluSerProA 380
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                                                                                                                                                   GluProIleAspAlaThrGlyPheIleAsnIleAsnSerLeuArgLeuLy
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alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 60736 SOFTWARE: Custom
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LOCATION: (112)..(157)
COTHER INFORMATION: Argininosuccinate synthase proteins domain identified by OTHER INFORMATION: eMATRIX, accession number BL00564C, p-value=1.000e-40, roother INFORMATION: 25.47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
LOCATION: (1)...(433)
OTHER INFORMATION: Xaa = X or *
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: DOMAIN
LOCATION: (8)..(315)
COTHER INFORMATION: harginosuccinate synthase domain identified by PFam, accession OTHER INFORMATION: name Arginosuc_synth, E-value=5.5e-151, PFam score of 481.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens FEATURE:
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                                                                                                                                                                                                                                                                                                                                      GTTTGTGGAGGAGTTCATCTGGCCGGCCATCCAGCCCAGCGCACTGTATG
CACTGGCCCCCAGATAAAGGTCATTGCTCCCTGGAGGATGCCTGAATTC
                                     AAACAAGTGGAAATCGCCCAGCGGGAGGGGGCCAAGTATGTCTCCCACGG
                                                                                                                                                                                                                                             AGGACCGCTACCTCCTGGGCACCTCTCTTGCCAGGCCCTGCATCGCCCGC
                                                                                                                                                                                                                                                                                                                                                                                                                              GCACTGAAGCTTGGGGCCAAAAAGGTGTTCATTGAGGATGTCAGCAGGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATCTGGCCAACATTGGCCAGAAGGAAGACTTCGAGGAAGCCAGGAAGAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTCGTGCATCCTCGTGTGGCTGAAGGAACAAGGCTATGACGTCATTGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MetSerSerLysGlySerValValLeuAlaTyrSerGlyGlyLeuAspTh
                                                                                                                                LysGlnValGluIleAlaGlnArgGluGlyAlaLysTyrValSerHisGl
                                                                                                                                                                                                                                                                                                              uPheValGluGluPheIleTrpProAlaIleGlnSerSerAlaLeuTyrG\\
                                                                                      CGCCACAGGAAAGGGGAACGATCAGGTCCGGTTTGAGCTCAGCTGCTACT
                                                                                                                                                                                                                        luAspArgTyrLeuLeuGlyThrPhePheAlaArgProCysIleAlaArg
                                                                                                                                                                                                                                                                                                                                                                                                       AlaLeuLysLeuGlyAlaLysLysValPheIleGluAspValSerArgGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Quality:
Ratio:
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1165 ACCGGGTTCATCAACATCAATTCCCTCAGGCTGAAG......GAATA 1205
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                                                                                                                                                                                                                                                                                                                                                                 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    334 laProGluCysGluLeuValGlyProCysLeuArgGlnSerProGlnGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   983 GCCCTGAGTGTGAATTTGTCCGCCACTGCATCGCCAAGTCC...CAGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            201 GlnAlaProProGlyLeuTyrThrLysThrGlnAspProAlaLysAlaPr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  267 rLeuThrSerTrpGluAsnArgPheHisTrpGluLeuLysSerArgGlyI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        234 luGlyGlyProThrPheLysAspGlyThrThrHisGlnThrPheLeuGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TACAACCGGTTCAAGGGCCGCAATGACCTGATGGAGTACGCAAAGCAACA 500
                                                                                          ProGlyPheIleGln...ThrSerIleSerLeuLysAlaGluGlyAsnTy
                                                                                                                                                                                                                                                                                                           GTACATCCTCGGCCGGGAGTCCCCA...CTGTCTCTTACAATGAGGAGC 1120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCTGGGCTTGAAATTTGCTGAGCTG...GTGTATACCGGTTTACGGCCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAACACCCCTGACATTCTCGAGATCGAGTTCAAAAAAAGGGGTCCCTGTGA
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rHisArgLeuProArgAlaLysValThrAlaGln
                                         TCATCGTCTC...CAGAGCAAGGTCACTGCCAAA 1236
                                                                                                                                                                                    euValLysHisGlyThrCysGlnGlyAspTyrGluProAsn***LeuPro 400
                                                                                                                                                                                                                        TGGTGAGCATGAACGTG...GCG
                                                                                                                                                                                                                                                                              sThrSerLeuGlyProGluValProHisCysSerLeuTyrAsnGluGluL
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yLeuGlyPheGluPheValGluLeuGlyValTyrArgPheSerGlyThrA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATCGAGGCCTTCACCATGGACCGGGAAGTGCGCAAAATC...AAACAAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTCTTCATGTACCTGAACGAAGTCGCGGGCAAGCATGGCGTGGGC...CG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TyrAsnArgPheLysGlyArgAsnAspLeuMetGluTyrAlaLysGlnHi
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1_documentation_block:

Sequence 49199, Application PC/TUS0108631
APPLICANT: Hyseq, Inc APPLICANT: Hyseq, Inc TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 21272-049 CURRENT APPLICATION NUMBER: PCT/US01/08631 CURRENT FILING DATE: 2001-03-30
55 €
PRIOR APPLICATION NUMBER: 09/649,167 PRIOR FILING DATE: 2000-08-23 NUMBER OF SEO ID NOS: 60736
SOFTWARE Custom SEQ ID NO 49199 LENGTH: 385
TYPE: PRT ORGANISM: Homo sapiens FEATURE:
KEY: DOMAIN TON: (7)(44)
222
LOCATION: (8)(333) OTHER INFORMATION: Arginosuccinate synthase domain identified by PFam, accession OTHER INFORMATION: name Arginosuc_synth, E-value=7.7e-145, PFam score of 461.9 CT-US01-08631-49199
lignment_scores: Quality: 1431.50 Length: 407 Ratio: 4.618 Gaps: 2 Percent Similarity: 76.167 Percent Identity: 70.762
lignment_block: US-09-775-693-1 x PCT-US01-08631-49199
Align seg 1/1 to: PCT-US01-08631-49199 from: 1 to: 385
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51 CTCGTGCATCCTCGTGTGGCTGAAGGAACAAGGCTATGACGTCATTGCCT 100
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151 GCACTGAAGCTTGGGGCCAAAAAGGTGTTCATTGAGGATGTCAGCAGGGA 200
201 GTTTGTGGAGGAGTTCATCTGGCCGGCCATCCAGTCCAG
251 AGGACCGCTACCTCCTGGGCACCTCTCTTGCCAGGCCCTGCATCGCCCCGC 300
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351 CGCCACAGGAAAGGGGAACGATCAGGTCCGGTTTGAGCTCAGCTGCTACT 400
PAFG

TCCCTCAG
GTGCAGGGT ValGlnGly
GGCCGGGAGI GlyTrpGlus
TGGAAGGGAA :: laGluGlyLy
CCCTGAGTGT rProGluCys
:
CTG
AGACATCG
ATGGCGTGGGCCG sGlyValGlyTy
AGACCTCCTT
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; Sequence 1235, Application US/60243468
; GENERAL INFORMATION:
; APPLICANT: Beasley, Ellen

seq_name: /cgn2_6/ptodata/2/paa/US60_COMB.pep:US-60-243-468-1235

ISOLATED HUMAN DRUG TARGET PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN DRUG TARGET PROTEINS,

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FITTLE OF INVENTION: ISOLATED HUMAN DRUG TARG
TITLE OF INVENTION: NUCLEIC ACID MOLECULES E
TITLE OF INVENTION: NUCLEIC ACID MOLECULES E
TITLE OF INVENTION: AND USES THEEOF
FILE REFERENCE: CL000929
CURRENT APPLICATION NUMBER: US/60/243,468
CURRENT FILING DATE: 2000-10-27
NUMBER OF SEQ ID NOS: 2121
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1235
SEQ ID NO 1235
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; ORGANISM: HUMAN
US-60-243-468-1235
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US-09-775-693-1 x US-60-243-468-1235
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                                                                                                                                                                               448
                                                                                                                                                                                                                                                        398
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                                                                                                                                            146
                                                                                                                                                                                                                   129
           548 AGAACCTCATGCACATCAGCTACGAGGCTGGAATCCTGGAGAACCCCCAAG 597
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATGTCCAGCAAAGGCTCCGTG...GTTCTGGCCTACAGTGGCGGCCTGGA 47
                                                                   CGGCGCCACAGGAAAGGGGAACGATCAGGTCCGGTTTGAGCTCAGCTGCT 397
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                                                                                                                                          ACTCACTGGCCCCCAGATAAAGGTCATTGCTCCCTGGAGGATGCCTGAA 447
                                                                                                                                                                                                                                                                                           gGlyAlaThrGlyGlu.....TyrGlnValArgPheGluLeuThrTrpT 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        laTyrLeuAlaAsnThrGlyGlnLysGluAspPheGluGluAlaArgLys 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCTATCTGGCCAACATTGGCCAGAAGGAAGACTTCGAGGAAGCCAGGAAG 147
luAsnLeuMetHisIleSerTyrGluAlaGlyIleLeuGluAsnProLys 195
                                                                                                                                                                               TTCTACAACCGGTTCAAGGGCCGCAATGACCTGATGGAGTACGCAAAGCA 497
                                                                                                                                                                                                                 yrSerLeuValProGlnIleLysGlyThrAlaProTrpArgMetProGlu 145
                                                                                                                                                                                                                                                                                                                                                                                                      CGCAAACAAGTGGAAATCGCCCAGCGGGGGGGGGGGCCAAGTATGTGTCCCA 347
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quality: 1390.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4.680
86.842
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Percent Identity: 81.287
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Quality: 1350.50
Ratio: 4.502
Percent Similarity: 86.455
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                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 486
LENGTH: 347
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Spier, General Application US/60212664
APPLICANT: Ladunga, Steve
                                                             Align seg 1/1 to: US-60-212-664-486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Greenberg, Simon
APPLICANT: Rabkin, Steven
APPLICANT: Wang, Yu
TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING H
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: CL000687
                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/60/212,664
CURRENT FILING DATE: 2000-06-20
                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 636
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        698 TGAAGGTGACCAACGTCAAGGATGGCACCCACCCAGCAGACCTCCTTGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    648 CCCCAACACCCCTGACATTCTCGAGATCGAGTTCAAAAAAGGGGTCCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           196 AsnGlnValProProAsp.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    598 AACCAAGCGCCTCCAGGTCTCTACACGAAGACCCCAGGCCCAAAGC | | | | | | | | | | | | | |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     898 TTCACCATGGACCGGGAAGTGCGCAAAATCAAACAAGGCCTGGGCTTGAA 947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       202 .....ArgValLysLysGlyValProV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      998 TTGTCCGCCACTGCATCGCCAAGTCC 1023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        948 ATTTGCTGAGCTGGTGTATACCGGTTTACGGCCTAGCCCTGAGTGTGAAT 997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     259 luThrProAlaGlyThrIleLeuTyrHisThrHisLeuAspIleLysAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           848 AGACCCCAGCAGCACCATCCTTTACCATGCTCATTTAGACATCGAGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     242 rAspIleValGluAsnArgPheThrGlyMetLysSerArgGlyTleTyrG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             798 TGACATCGTGGAGAACCGCTTCATTGGAATGAAGTCCCGAGGTATCTACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      226 PhePheMetTyrLeuAsnGluValAlaAspLysHisGlyValGlyCysTh
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PheThrMetAspTrpGluValCysLysIleLysGlnGlyLeuGlyLeuLy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Spier, Gene
Greenberg, Simon
Rabkin, Steven
                                                                                                                                                                       Percent Identity: 78.386
                                                                    from: 1
                                                                                                                                                                                                                 Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ENCODING HUMAN SECRETED PROTEINS, AND
                                                               to: 347
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851 CCCCAGCAGCACCATCCTTTACCATGCTCATTTAGACATCGAGGCCTTC 900
                                                                                                                                                                               801 CATCGTGGAGAACCGCTTCATTGGAATGAAGTCCCGGAGGTATCTACGAGA 850
                                           901 ACCATGGACCGGGAAGTGCGCAAAATCAAACAAGGCCTGGGCTTGAAATT 950
                                                                                                                                                                                                                                                                                                                                                                   204 ysValThrAsnValLysAspSerAlaThrHisGlnThrSerLeuGluLeu 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    601 CAAGCGCCTCCAGGTCTCTACACGAAGACCCAGGGACCCAGCCAAAGCCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         451 TACAACCGGTTCAAGGGCCGCAATGACCTGATGGAGTACGCAAAGCAACA 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       401 CACTGGCCCCCAGATAAAGGTCATTGCTCCCTGGAGGATGCCTGAATTC 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      351 CGCCACAGGAAAGGGGAACGATCAGGTCCGGTTTGAGCTCAGCTGCTACT 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     251 AGGACCGCTACCTCCTGGGCACCTCTCTGCCAGGCCCTGCATCGCCCGC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                151 GCACTGAAGCTTGGGGCCAAAAAGGTGTTCATTGAGGATGTCAGCAGGGA 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       101 ATCTGGCCAACATTGGCCAGAAGGAAGACTTCGAGGAAGCCAGGAAGAAG 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84 luAspArgTyrLeuLeuGlyThrSerLeuAlaArgProCysIleThrHis 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51 AlaLeuLysProGlyAlaLysLysMetLeuIleGluAspValAsnArgGl 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ThrMetTyrArgGluValHisLysIleLysGlnCysArgGlyLeuLysPh
                                                                                                                                                                                                                                                                       laProAlaGlyThrIleLeuCysTyrAlaHisLeuAspIleGluAlaPhe
                                                                                                                                                                                                                                                                                                                                                                                                                AGGTGACCAACGTCAAGGATGGCACCACCACCAGACCTCCTTGGAGCTC 750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAACACCCCTGACATTCTCGAGATCGAGTTCAAAAAAGGGGTCCCTGTGA 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CGGGATTCCCATCCCGGTCACTCCCAAGAACCCGTGGAGCATGGATGAGA 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                              oAsnThrProAspIleLeuGluIleGluPheLysLysGlyValProValL 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GlnAlaProProAlaLeuTyrThrLysThrGlnAspProAlaLysThrPr 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               snLeuMetHisIleSerCysGluAlaGlyIleLeuGluAsnProGluAsn 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gGlyIleProThrProValThrProLysAsnProTrpSerMetAspGluA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAACAAGTGGAAATCGCCCAGCGGGAGGGGGCCAAGTATGTGTCCCACGG 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          UPheValGluGluPheIleTrpProAlaMetGlnSerSerThrLeuTyrG
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alignment_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_name: /cgn2_6/ptodata/2/paa/US60_COMB.pep:US-60-216-770-97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-775-693-1 x US-60-216-770-97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 97, Application US/60216770
GENERAL INFORMATION:
APPLICANT: Ladunga, Steven
APPLICANT: Spier, Eugene
APPLICANT: Greenberg, Simon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 97
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APPLICANT:
APPLICANT:
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CURRENT FILING DATE: 2000-07-07
NUMBER OF SEQ ID NOS: 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: BONAZZÍ, VÍVÍCH
TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: CL000727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 347
TYPE: PRT
151 GCACTGAAGCTTGGGGCCAAAAAGGTGTTCATTGAGGATGTCAGCAGGGA 200
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                                                                                                                                                                                                                                          304 ValAsnLeuSerAlaThrAlaSerProSerProArgSer 316
                                                                                                                                                             67 uPheValGluGluPheIleTrpProAlaMetGlnSerSerThrLeuTyrG
                                                                                                                                                                                                                                                                                                                                                                                                     17 rPheCysIleLeuValTrpLeuLysGluGlnGlyTyrAspValIleAlaT
                                                                                                                                                                                                                                                                                                                                                                                                                                             51 CTCGTGCATCCTCGTGTGGCTGAAGGAACAAGGCTATGACGTCATTGCCT 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MetSerSerLysGlySerIleValLeuAlaCysSerGlySerLeuAspTh 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ATGTCCAGCAAAGGCTCCGTGGTTCTGGCCTACAGTGGCGGCCTGGACAC 50
                                                                                                    AGGACCGCTACCTCCTGGGCACCTCTCTTTGCCAGGCCCTGCATCGCCCGC 300
                                                                               luAspArgTyrLeuLeuGlyThrSerLeuAlaArgProCysIleThrHis 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTGAATTTGTCCGCCACTGCATCGCCAAGTCCCAGGAGC 1030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quality: 1350.50
Ratio: 4.502
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                                                                                                                                                                                                                                                                                                                                                                                                                            Wang, Yu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rabkin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   86.455
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Identity: 78.386
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seq_name: /cgn2_6/ptodata/2/paa/PCTUS_COMB.pep:PCT-US01-08631-49202
                                                                                                                                                                                                                                                                                          seq_documentation_block:
                                                                                                                                                                                     Sequence 49202, Application PC/TUS0108631
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 21272-049
NUMBER OF SEQ ID NOS: 60736
SOFTWARE: Custom
SEQ ID NO 49202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: 09/540,217
PRIOR FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR FILING DATE: 2000-08-23
                                                                                                                                                 CURRENT APPLICATION NUMBER: PCT/US01/08631
CURRENT FILING DATE: 2001-03-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       401 CACTGGCCCCCCAGATAAAGGTCATTGCTCCCTGGAGGATGCCTGAATTC 450
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               501 CGGGATTCCCCATCCCGGTCACTCCCAAGAACCCCGTGGAGCATGGATGAGA 550
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          801 CATCGTGGAGAACCGCTTCATTGGAATGAAGTCCCGAGGTATCTACGAGA 850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          751 TTCATGTACCTGAACGAAGTCGCGGGCAAGCATGGCGTGGGCCGTATTGA 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           901 ACCATGGACCGGGAAGTGCGCAAAATCAAACAAGGCCTGGGCTTGAAATT 950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    304 ValAsnLeuSerAlaThrAlaSerProSerProArgSer 316
                                                                                                                                                                                                                                                                                                                                                                                                                          992 GTGAATTTGTCCGCCACTGCATCGCCAAGTCCCCAGGAGC 1030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        951 TGCTGAGCTGGTGTATACCGGTTTAC......GGCCTAGCCCTGAGT 991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   271 ThrMetTyrArgGluValHisLysIleLysGlnCysArgGlyLeuLysPh 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   snLeuMetHisIleSerCysGluAlaGlyIleLeuGluAsnProGluAsn 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAACACCCCTGACATTCTCGAGATCGAGTTCAAAAAAAGGGGTCCCTGTGA 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACCTCATGCACATCAGCTACGAGGCTGGAATCCTGGAGAACCCCAAGAAC 600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       aIleValGluAsnArgPheIleGlyThrLysSerArgGlyIleTyrArgA 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCCCAGCAGGCACCATCCTTTACCATGCTCATTTAGACATCGAGGCCTTC 900
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alignment_block:
US-09-775-693-1 x PCT-US01-08631-49202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Align seg 1/1 to: PCT-US01-08631-49202 from: 1 to:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Arginosuccinate synthase domain identified by PFam, accession OTHER INFORMATION: name Arginosuc_synth, E-value=6.4e-68, PFam score of 217.6 NAME/KEY: misc_feature LOCATION: (1)...(487) OTHER INFORMATION: Xaa = X or * as defined in Table 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Argininosuccinate synthase proteins domain identified by OTHER INFORMATION: eMATRIX, accession number BL00564A, p-value=2.800e-37, raw sco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: DOMAIN
LOCATION: (24)..(272)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: 19.93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               101 ATCTGGCCAACATTGGCCAGAAGGAAGACTTCGAGGAAGCCAGGAAGAAG 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               151 GCACTGAAGCTTGGGGCCAAAAAGGTGTTCATTGAGGATGTCAGCAGGGA 200
                                                                                                                                                                                         389 TCAGCTGCTACTGACCGCCCCCAGATAAAGGTCATTGCTCCCTGGAGG 438
                                                                                                                                                                                                                                                                                      133 lValProThrGlyAlaThrGlyLysGlyAsnGluGlnValArgPheGluL 150
                                                                                                                                                                                                                                                                                                                                                                                     117 AlaArgLysGlnValGlyAsnSerProSerGlyArgGlyAlaLysTyrVa 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100 yrGluAspArgTyrLeuProGlyHisLeuSerLeuProGlyProCysIle 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 248 ATGAGGACCGCTACCTCCTGGGC...ACCTCTCTTGCCAGGCCCTGCATC 294
|:::||
183 rGlyLysAlaThrLeuGlyPheProIleProValThrProLysAsnProT
                                                                                                 167
                                                                                                                                                                                                                                                                                                                                       340 GTGTCCCACGGCGCCACAGGAAAGGGGAACGATCAGGTCCGGTTTGAGC 388
                                                                                                                                                                                                                                                                                                                                                                                                                                    295 GCCCGCAAACAAGTG...GAAATCGCCCAGCGGGAGGGGGCCAAGTAT.. 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67 AlaLeuLysLeuGlyAlaLysLysValPheIleGluAspValSerArgGl 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33 rSerCysIleLeuValTrpLeuLysGluGlnGlyTyrAspValIleAlaT 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51 CTCGTGCATCCTCGTGTGGCTGAAGGAACAAGGCTATGACGTCATTGCCT 100
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                                              489 CGCAAAGCAACAC...GGGATTCCCCATCCCGGTCACTCCCAAGAACCCCGT 535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  83 uPheValGluGluPheIleTrpProAlaIleGlnValGlnAlaHisLeuT 100
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                                                                                               MetProGluPheTyrAsnArgPheLysGlyArgAsnAspLeuMetGluTy
                                                                                                                                           ATGCCTGAATTCTACAACCGGTTCAAGGGCCGCAATGACCTGATGGAGTA 488
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Ratio: 3.670
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                                                                                                                                                                                                                                                                                                                     percent Identity: 69.438
                    200
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seq_documentation_block:
Sequence 544, Application US/60185362
GENERAL INFORMATION:
APPLICANT: Bonazzi, viven
TITLE OF INVENTION: ISOLATED HUMAN DRUG TARGET PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN DRUG TARGET PROTEINS,
TITLE OF INVENTION: AND USES THEREOF
                                                                                                                                                                                                          seq_name: /cgn2_6/ptodata/2/paa/US60_COMB.pep:US-60-185-362-544
                                                                                                                                                                                                                                                                                             1205 ATCATCGTCTC...CAGAGCAAGGTCACTGCCAAA 1236
                                                                                                                                                                                                                                                                                                                                                                                                          1164 CACCGGGTTCATCAACATCAATTCCCTCAGGCTGAAG......GAAT 1204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1120 CTGGTGAGCATGAACGTG...CAGGGTGATTAT...GAGCCAACTGATGC 1163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1079 TCCTC...GGCCGGGAGTCCCCA......CTGTCTCTCTACAATGAGGAG 1119
                                                                                                                                                                                                                                                               447 yrHisArgLeuProArgAlaLysValThrCysGln 458
                                                                                                                                                                                                                                                                                                                                                               430 yHisArgGlySerSerLysHisGlnIleProPheLysAlaGluGlyAsnT 447
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  397 leLeuSerGlyArgGluIleProHisCysLeuLeuThrMetArgGlu 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  380 yLysGlyLysValGlnValValArgSerPheLysGlyProGlnValTyrI 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       366 ......CysProProThrGlyIleAlaLysValProArgLysProSerGl 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       350 luLeuValTyrThrGlyPheProAlaGlnAlaProGluCysGluPhe... 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       956 AGCTGGTGTATACCGGTTTA...CGGCCTAGCCCTGAGTGTGAATTTGTC 1002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          333 gGlySerCysGlyLysIleLysGlnGlyProGlyAlaTrpLysPheAlaG 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          317 SerPheTyrHisAlaHisLeuAspIleArgGlyLeuSerProTrpAspAr 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          865 ATCCTTTACCATGCTCATTTAGACATCGAGGCCTTCACC...ATGGACCG 911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             824 GAATGAAGTCC...CGAGGTATCTAC...GAGACCCCAGCAGGC...ACC 864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               283 yLysHisGlyArgArgAlaValPheAspIleValGluAsnArgPheIleG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             777 CAAGCATGGCGTGGGCCGTATT...GACATCGTGGAGAACCGCTTCATTG 823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               267 ThrHisGlnThrPheLeuGluLeuPheMetTyrLeuAsnGluValAlaGl 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  727 ACCCACCAGACCTCCTTGGAGCTCTTCATGTACCTGAACGAAGTCGCGGG 776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  250 heLysLysGlyValProValGluGlyGlyProThrPheLysAspGlyThr 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               680 TCAAAAAAGGGTTCCCTGTGAAG...GTGACCAACGTCAAGGATGGCACC 726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  636 CCCAGCCAAAGCCCCCAACACCCCT...GACATTCTC...GAGATCGAGT 679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     586 GAGAACCCCAAGAACCAAGCGCCTCCAGGTCTCTACACGAAGACCCCAGGA 635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     200 rpSerMetAspGluAsnLeuMetHisIleSerTyrGluAlaGlyIleLeu 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       G...GAAGTGCGCAAAATCAAACAAGGCCTGGGCTTG...AAATTTGCTG 955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             lyAsn***SerProArgGlyIleLeuArgArgThrProAlaGlyHisHis 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGAGCATGGATGAGAACCTCATGCACATCAGCTACGAGGCTGGAATCCTG 585
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alignment_block:
US-09-775-693-1 x US-60-185-362-544
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CRGANISM: HUMAN

FERATURE:

NAME/KEY: VARIANT

LOCATION: (1)...(299)

OTHER INFORMATION: Xaa = Any Amino
US-60-185-362-544
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1 to: US-60-185-362-544 from: 1 to: 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity: 91.333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: CL000285
CURRENT APPLICATION NUMBER: US/60/185,362
CURRENT FILING DATE: 2000-02-28
NUMBER OF SEQ ID NOS: 836
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 544
LENGTH: 299
166 gPheIleGluMetLysSer***GlyIleCysLysThrProAlaGlyThrI 183
                                         866 TCCTTTACCATGCTCATTTAGACATCGAGGCCTTCACCATGGACCGGGAA 915
                                                                                                                                     816 CTTCATTGGAATGAAGTCCCGAGGTATCTACGAGACCCCAGCAGGCACCA 865
                                                                                                                                                                            150 GluValAlaGlyLysHisSerValGlyHisTleAspTleValGluAsnAr 166
                                                                                                                                                                                                                          766 GAAGTCGCGGGCAAGCATGGCGTGGGCCGTATTGACATCGTGGAGAACCG 815
                                                                                                                                                                                                                                                                        716 AGGATGGCACCACCACCAGACCTCCTTGGAGCTCTTCATGTACCTGAAC 765
                                                                                                                                                                                                                                                                                                                                                             117 ePheLysThrGlu...LysLysGlyValProValLysValThrSerIleL 133
                                                                                                                                                                                                                                                                                                                                                                                                              666 TCTCGAGATCGAGTTCAAAAAAGGGGTCCCTGTGAAGGTGACCAACGTCA 715
                                                                                                                                                                                                                                                                                                                                                                                                                                                              101 LeuTyrMetLysIleGlnAspLeuAlaLysAlaProAsnThrProAsnIl 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          616 CTCTACACGAAGACCCAGGACCCAGCCAAAGCCCCCAACACCCCTGACAT 665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 566 GCTACGAGGCTGGAATCCTGGAGAACCCCAAGAACCAAGCGCCTCCAGGT 615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           516 GGTCACTCCCAAGAACCCGTGGAGCATGGATGAGAACCTCATGCACATCA 565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     466 GGCCGCAATGACCTGATGGAGTACGCAAAGCAACACGGGATTCCCCATCCC 515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             416 TAAAGGTCATTGCTCCCTGGAGGATGCCTGAATTCTACAACCGGTTCAAG 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                316 GCCCAGCGGGGGGGGCCAAGTATGTGTCCCACGGCGCCACAGGAAAGGG 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84 erHisGluAlaGlyIleLeuGluAsnProLysAsnGlnAlaProSerGly 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67 oValThrLeuLysHisProTrpAsnMetAspGluAsnLeuMetHisIleS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51 GlyArgSerAspLeuMetGluTyrAlaGluLysHisGlyIleProIlePr 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34 leLysValIleAlaProGlyArgIleProGluPheTyrAsnGlnSerLys 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17 yAsnAspGlnValTrpPheGluLeuAlaCysTyrSerLeuAlaProGlnI 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Quality: 1207.50
Ratio: 4.407
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1166	1116	1066	1016	966	916
283	266	250	233	216	200
CCGGGTTCATCAACATCAATTCCCTCAGGCTGAAGGAATATCATCGTCTC	GGAGCTGGTGAGCATGAACGTGCAGGGTGATTATGAGCCAACTGATGCCA	GGCCAGGTGTACATCCTCGGCCGGGAGTCCCCACTGTCTCTCTACAATGA	CCAAGTCCCAGGAGCGAGTGGAAGGGGAAAGTGCAGGTGTCCGTCC	TACCGGTTTACGGCCTAGCCCTGAGTGTGAATTTGTCCGCCACTGCATCG	GTGCGCAAAATCAAACAAGGCCTGGGCTTGAAATTTGCTGAGCTGGTGTA
1215	1165	1115	1065	1015	965
299	283	266	249	233	216

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183.93 184.73 184.27 185.41 187.74

0.0034 0.0039 0.0048 0.0054 0.0053

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Sequence_list:

Sequence_list:

Sequence_Compa_Seprence_Comps_pepics_60-9881-338-87 + 2123.00 3133.67 2.1e-167 41
//cgn2_Seprodata/2/pea/Visio_New_Comb.pepics_60-9881-338-87 + 2123.00 3133.67 2.1e-167 41
//cgn2_Seprodata/2/pea/Visio_New_Comb.pepics_60-940-187-7014-2036.00 3000.91 3.6e-160 5
//cgn2_Seprodata/2/pea/Visio_New_Comb.pepics_60-340-187-7014-2036.00 3000.91 3.6e-160 5
//cgn2_Seprodata/2/pea/Visio_New_Comb.pepics_60-340-187-7014-2036.00 3000.91 3.6e-160 3.6c-160 1.000 5
//cgn2_Seprodata/2/pea/Visio_New_Comb.pepics_60-340-187-7015-20-340-180-35 3.6e-60 3.6c-36 1.000 3000.91 3.6e-60 3.6c-36 3.6c-30 1.000 3000.91 3.6c-36 3.6c-30 1.000 3.6c-36 3.6c-30 1.000 3000.91 3.6c-36 3.6c-30 1.000 3000.91 3.6c-30 3.6c
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Sequence
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Database sequences: 216105
Database length: 44922408
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-Q-/cgn2_1/USPTO_spool/US99775693/runat_12022002_124153_1396/app_query.fasta_1.1315
-Q-/cgn2_1/USPTO_spool/US99775693/runat_12022002_124153_1396/app_query.fasta_1.1315
-DB-Pending_Patents_AA_wew -OPWT-fastan -SUFFIX-rapn
-GAPOD-12.000 -GAPEXT-4.000 -MINMATCH-0.100 -LOOPCL-0.000
-LOOPEXT=0.000 -QGAPOD+4.500 -QGAPEXT-0.050 -XGAPOD-10.000
-XGAPEXT=0.500 -FGAPOD+6.000 -FGAPEXT=7.000 -YGAPOD-10.000
-YGAPEXT=0.500 -DELOP-6.000 -DELEXT=7.000 -START=1
-MATRIX-bLOSUM62 -TRANS-human40.cdi -LIST-45 -DOCALIGN=200
-THE_SCORE-PCt -THE_MAX=100 -THE_MIN-0 -ALIGN=15 -MODE-LOCAL
-OUTFMT-pfs -NORM-ext -MINLEN-0 -MAXLEN-200000000
-USER-US09775693_@CGN1_1_44 -NCPU=6 -ICPU=3 -LONGLOG -NO_XLPXY
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    Quality:
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LENGTH: 412
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                                                                                                                                                                                                                                   117
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                                                  Ratio:
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seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-775-693-1 x US-09-981-353-87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 87, Application US/09981353 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/981,353
CURRENT FILING DATE: 2001-10-11
NUMBER OF SEQ ID NOS: 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Lasek, Amy W. APPLICANT: Jones, David A. TITLE OF INVENTION: GENES EXPRESSED IN COLON CANCER FILE REFERENCE: PA-0038 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PERL Program
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Incyte ID
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401 CACTGGCCCCCCAGATAAAGGTCATTGCTCCCTGGAGGATGCCTGAATTC
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    APPLICANT: Wang, Zhiwei
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            751 TTCATGTACCTGAACGAAGTCGCGGGCAAGCATGGCGTGGGCGTATTGA 800
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                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: PCT/US01/14827
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PRIOR PLIANG DATE: 2000-01-21
PRIOR APPLICATION NUMBER: US 09/552,317
PRIOR FILING DATE: 2000-04-25
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CURRENT FILING DATE: 2001-12-12
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TITLE OF INVENTION: Novel Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 813
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 09/770,160 FILING DATE: 2001-01-26 APPLICATION NUMBER: PCT/US01/08656 FILING DATE: 2001-04-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 2000-08-23
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FILING DATE: 2000-02-03
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FILING DATE: 2000-04-27
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FILING DATE: 2001-02-05
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; Sequence 1176, Applica
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Novel Nucleic Acids and TITLE OF INVENTION: Polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 09/488,725
PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: US 09/552,317
PRIOR ETILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: PCT/US00/35017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Tang, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 2000-01-25
PRIOR APPLICATION NUMBER: PCT/US01/02623
PRIOR FILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: US 09/496,914
PRIOR APPLICATION NUMBER: US 09/496,914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/60/340,187 CURRENT FILING DATE: 2001-12-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1051 GTGTCCGTCCTCAAGGGCCAGGTGTACATCCTCGGCCGGGAGTCCCCACT 1100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1001 TCCGCCACTGCATCGCCAAGTCCCAGGAGCGAGTGGAAGGGAAAGTGCAG 1050
                                                                                             PRIOR
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                                                                                                                                                                                                                                                           PRIOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 443 uSerLeuTyrAsnGluGluLeuValSerMetAsnValGlnGlyAspTyrG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           393 eAlaGluLeuValTyrThrGlyPheTrpHisSerProGluCysGluPheV 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   951 TGCTGAGCTGGTGTATACCGGGTTTACGGCCTAGCCCTGAGTGTGAATTTG 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                460 luProThrAspAlaThrGlyPheIleAsnIleLysPheLeu 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 2001-02-26
APPLICATION NUMBER: US 09/519,705
FILING DATE: 2000-03-07
                                                                                                                                                                                                                                                                                               FILING DATE: 2001-02-05
APPLICATION NUMBER: US 09/515,126
FILING DATE: 2000-02-28
                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: PCT/US01/03800 FILING DATE: 2001-02-05
                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 09/560,875 FILING DATE: 2000-04-27
                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 2000-02-03
                                                                                                                                                                                                                    APPLICATION NUMBER: PCT/US01/04927 FILING DATE: 2001-02-26
                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 09/577,409 FILING DATE: 2000-05-18
                                                                                                                                    APPLICATION NUMBER: US 09/574,454 FILING DATE: 2000-05-19
              FILING DATE: 2000-03-31
APPLICATION NUMBER: US 09/649,167
FILING DATE: 2000-08-23
                                                                            APPLICATION NUMBER:
                                                                                                                  APPLICATION NUMBER: PCT/US01/04941
APPLICATION NUMBER: PCT/US01/08631
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Wang, Jian-Rui
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Boyle, Bryan J
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                                                                                                 2001-03-05
                                                                                US 09/540,217
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PRIOR APPLICATION NUMBER: PCT/US01/0856
PRIOR FILING DATE: 2001-04-18
PRIOR APPLICATION NUMBER: US 09/577,408
PRIOR FILING DATE: 2000-05-18
PRIOR APPLICATION NUMBER: PCT/US01/14827
PRIOR FILING DATE: 2001-05-16
NUMBER OF SEQ ID NOS: 1192
SOFTWARE: Pt_FL_genes Version 6.0
SEQ ID NO 1176
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US-09-775-693-1 x US-60-340-187-1176
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PRIOR APPLICATION NUMBER: US 09/770,160
PRIOR FILING DATE: 2001-01-26
                       451 TACAACCGGTTCAAGGGCCGCAATGACCTGATGGAGTACGCAAAGCAACA 500
                                                                                      134 erLeuAlaProGlnIleLysValIleAlaProTrpArgMetProGluPhe 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 09/552,929
                                                                                                                                 401 CACTGGCCCCCCAGATAAAGGTCATTGCTCCCTGGAGGATGCCTGAATTC 450
                                                                                                                                                                             117 yAlaThrGlyLysGlyAsnAspGlnValArgPheGluLeuSerCysTyrS
                                                                                                                                                                                                                     351 CGCCACAGGAAAGGGGAACGATCAGGTCCGGTTTGAGCTCAGCTGCTACT 400
                                                                                                                                                                                                                                                                  FEATURE:

NAME/KEY: misc_feature
LOCATION: (1)...(433)
OTHER INFORMATION: Xaa = any amino acid or symbol as shown in the table 8 as set
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                                                                                                                                                                                                                                                                                                            301 AAACAAGTGGAAATCGCCCAGCGGGGGGGGGGCCAAGTATGTGTCCCACGG 350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  101 ATCTGGCCAACATTGGCCAGAAGGAAGACTTCGAGGAAGCCAGGAAGAAG 150
                                                                                                                                                                                                                                                                                                                                                         84 luAspArgTyrLeuLeuGlyThrPhePheAlaArgProCysIleAlaArg
                                                                                                                                                                                                                                                                                                                                                                                                                                               67 uPheValGluGluPheIleTrpProAlaIleGlnSerSerAlaLeuTyrG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51 CTCGTGCATCCTCGTGTGGCTGAAGGAACAAGGCTATGACGTCATTGCCT 100
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TyrAsnArgPheLysGlyArgAsnAspLeuMetGluTyrAlaLysGlnHi 167
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Ratio: 4.310
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1206 TCATCGTCTC...CAGAGCAAGGTCACTGCCAAA 1236
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                                                                                                                                                                                                                                                        1121 TGGTGAGCATGAACGTG...CAGGGTGATTATGAGCCAACTGAT...GCC 116
                                                                                                                                                                                                                                                                                                                                         1074 GTACATCCTCGGCCGGGAGTCCCCA...CTGTCTCTACAATGAGGAGC 1120
416 rHisArgLeuProArgAlaLysValThrAlaGln 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1030 CGAGTGGAAGGGAAA...GTGCAGGTGTCCGTCCTCAAGGGC...CAGGT 1073
                                                                                                401 ProGlyPheIleGln...ThrSerIleSerLeuLysAlaGluGlyAsnTy 416
                                                                                                                                                                                                         384 euValLysHisGlyThrCysGlnGlyAspTyrGluProAsn***LeuPro 400
                                                                                                                                                                                                                                                                                                             367 sThrSerLeuGlyProGluValProHisCysSerLeuTyrAsnGluGluL 384
                                                                                                                                                                                                                                                                                                                                                                                                                   351 ArgValGluGlyLysSerAlaGlyValProSerLeuLysGlyProArgCy 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       334 laProGluCysGluLeuValGlyProCysLeuArgGlnSerProGlnGlu 350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             317 yLeuGlyPheGluPheValGluLeuGlyValTyrArgPheSerGlyThrA 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    842 TCTACGAGACCCCA...GCAGGCACCATCCTTTACCATTGTCATTTAGAC 888
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   889 ATCGAGGCCTTCACCATGGACCGGGAAGTGCGCAAAATC...AAACAAGG 935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           267 rLeuThrSerTrpGluAsnArgPheHisTrpGluLeuLysSerArgGlyI 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            795 TATTGACATCGTGGAGAACCGCTTC...ATTGGAATGAAGTCCCGAGGTA 841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           251 LeuPheMetTyrLeuAsnGluValAlaGlyLysHisGlyValGlyProTy 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   748 CTCTTCATGTACCTGAACGAAGTCGCGGGCAAGCATGGCGTGGGC...CG 794
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       551 ACCTCATGCACATCAGCTACGAGGCTGGAATCCTGGAGAACCCCCAAGAAC 600
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seq_documentation_block:

Sequence 9692, Appli GENERAL INFORMATION:

Application US/10015127

APPLICANT: Bower, Stanley G. APPLICANT: Hinkle, Gregory J. APPLICANT: Slater, Steven C.

seq_name: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep:US-10-015-127-9692

for

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; TYPE: PRT ; ORGANISM: Sphingomonas elodea US-10-015-127-9692
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US-09-775-693-1 x US-10-015-127-9692
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Percent Similarity: 75.490
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PRIOR FILING DATE: 2000-11-22
NUMBER OF SEQ ID NOS: 14357
SEQ ID NO 9692
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CURRENT FILING DATE: 2001-10-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 405
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                                                                                                                                                                                                                                                                                                                                                                               386 AGCTCAGCTGCTACTCACTGGCCCCCCAGATAAAGGTCATTGCTCCCTGG 435
                                                                                                                                                                                                                                                                                                                                                                                                                       116 palaValSerHisGlyAlaThrGlyLysGlyAsnAspGlnValArgPheG 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       336 GTATGTGTCCCACGGCGCCACAGGAAAGGGGAACGATCAGGTCCGGTTTG 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 286 CCCTGCATCGCCCGCAAACAAGTGGAAATCGCCCAGCGGGAGGGGGCCAA 335
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                                                                                                                                                                                      486 GTACGCAAAGCAACACGGGATTCCCATCCCGGTCACTCCCAAG.....A 529
                                                                                                                                                                                                                                                                                436 AGGATGCCTGAATTCTACAACCGGTTCAAGGGCCGCAATGACCTGATGGA 485
                                                                                                                                                                                                                                                                                                                             66 uAspValArgGluGluPheValLysAspTyrValPheProMetMetArgA 83
                                                                                                                                                                                                                                      150 ArgGluTrpAspLeuThrSerArgThrLys.....LeuIleGl 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                580 ATCCTGGAGAACCCCAAGAACCAAGCGCCTCCAGGTCTCTACACGAAGAC 629
                                                                                            530 ACCCGTGGAGCATGGATGAGAACCTCATGCACCATCAGCTACGAGGCTGGA 579
                                                                                                                                         162 uPheAlaGluSerHisGlnIleProValThrLysAspLysArgGlyGluS 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ATGTCCAGCAAA...GGCTCCGTGGTTCTGGCCTACAGTGGCGGCCTGGA 47
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|ProLeuIleAlaLysArgGlnIleGluIleAlaLysLeuValGlyAlaAs 116
                                                  ::|||:::||| ||| |||||||:::||| ||| |||:::
erProPheSerThrAspAlaAsnLeuLeuHisThrSerSerGluGlyLys 195
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seq_documentation_block:
    Sequence 79358, Application US/09708427
    GENERAL INFORMATION:
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                                      CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: PatentIn version 3.1
SEQ ID NO 79358
                                                                                                                                                                                   TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID TITLE OF INVENTION: THEREBY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 :::||||||:::::|||
196 ValLeuGluAspProTrpGluGluValProAspTyrValTyrSerArgTh 212
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                                                                                                                                                               FILE REFERENCE: 2750-1243P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  730 CACCAGACCTCCTTGGAGCTCTTCATGTACCTGAACGAAGTCGCGGGCAA 779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 680 TCAAAAAAGGGGTCCCTGTGAAGGTGACCAACGTCAAGGATGGCACCACC 729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             212 rValAsnProGluAspAlaProAspMetProGluThrIleThrIleAspP 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1130 TG...AACGTGCAGGGTGATTATGAGCCAACTGATGCCACCGGGTTCATC 1176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    830 AGTCCCGAGGTATCTACGAGACCCCAGCAGGCACCATCCTTTACCATGCT 879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   780 GCATGGCGTGGGCCGTATTGACATCGTGGAGAACCGCTTCATTGGAATGA 829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241 AlaMetSerProAlaThrLeuLeuThrAlaLeuAsnGluLeuGlyArgLy 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                           1177 AACATCAATTCCCTCAGGCTGAAG 1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       930 ACAAGGCCTGGGCTTGAAATTTGCTGAGCTGGTGTATACCGGTTTTACGGC 979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        880 CATTTAGACATCGAGGCCTTCACCATGGACCGGGAAGTGCGCAAAATCAA 929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      257 shisGlyIleGlyArgLeuAspLeuValGluAsnArgPheValGlyMetL 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               324 heSerProGluArgGluMetLeuGlnAlaAlaValAspTyrSerGlnGlu 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          980 CTAGCCCTGAGTGTGAATTTGTCCGCCACTGCATCGCCAAGTCCCAGGAG 1029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          291 HisArgGlyIleGluGlnIleThrLeuAspArgGlyAlaAlaHisLeuLy 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  357 lThrGlyArgLysSerProTyrSerLeuTyrSerGluLysValValThrP 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                341 LysValThrGlyThrValArgLeuLysLeuTyrLysGlySerValIleVa 357
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                           391 LysLeuAsnAlaLeuArgLeuArg 398
                       LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   heGluArgGlyAspGlyValAlaLeuAsnGly......Gln 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sAspGluLeuAlaProArgTyrAlaGluLeuIleTyrAsnGlyPheTrpP 324
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LOCATION: 1..425
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature

ORGANISM: Zea mays subsp. mays

NAME/KEY: misc_feature

FEATURE:

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alignment_block:
us-09-775-693-1 x Us-09-708-427-79358
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; OTHER INFORMATION: Ceres Seq. ID 1965189
US-09-708-427-79358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Align seg 1/1 to: US-09-708-427-79358 from: 1 to: 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Quality: 866.50
Ratio: 2.947
Percent Similarity: 74.809
242 uTyrLeuGluIleGlyTleIleAlaGlyValProValSerIle...AsnG 258
                                                                                                          663 CATTCTCGAGATCGAGTTCAAAAAAGGGGTCCCTGTGAAGGTGACCAACG 712
                                                                                                                                                   226 AspMetTyrMetMetSerIleAlaProGluAsnAlaProSerLysProGl 242
                                                                                                                                                                                             613 GGTCTCTACACGAAGACCCAGGACCCAGCCAAAGCCCCCAACACCCCTGA 662
                                                                                                                                                                                                                                      209 euSerHisGluGlyAspIleLeuGluAspProAlaAsnGluProLysGlu 225
                                                                                                                                                                                                                                                               192 lProvalSerLysLysSerIleTyrSerArgAspArgAsnLeuTrpHisL 209
                                                                                                                                                                                                                                                                                                                                                                   513 CCCGGTCACTCCCAAGAACCCGTGGAGCATGGATGAGAACCTCATGCACA 562
                                                                                                                                                                                                                                                                                                                                                                                                            176 ThrGlyArgGluAspAlaIleGluTyrAlaLysLysHisAsnValDroVa 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                          463 AAGGGCCGCAATGACCTGATGGAGTACGCAAAGCAACACGGGGATTCCCCAT 512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    163 luLeuLysValValalabroTrpArgGluTrpAsp.......ile 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         413 AGATAAAGGTCATTGCTCCCTGGAGGATGCCTGAATTCTACAACCGGTTC 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          130 ValalaLysGluValGlyAlaAspAlaValAlaHisGlyCysThrGlyLy 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     313 ATCGCCCAGCGGGAGGGGCCAAGTATGTGTCCCACGGCGCCACAGGAAA 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             263 TCCTGGGCACCTCTCTTGCCAGGCCCTGCATCGCCCGCAAACAAGTGGAA 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              213 GTTCATCTGGCCGGCCATCCAGTCCAGCGCACTGTATGAGGACCGCTACC 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 163 GGGGCCAAAAAGGTGTTCATTGAGGATGTCAGCAGGGAGTTTGTGGAGGA 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      116 GCCAGAAGGAA...GACTTCGAGGAAGCCAGGAAGAAGGCACTGAAGCTT 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96 uTyrIleTyrProCysLeuArgAlaGlyAlaValTyrGluArgLysTyrL 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         80 GlyAlaCysGlnLeuValValLysAspLeuLysGluGluPheValSerGl 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63 lyGlnGlyAlaIleGluLeuGluGlyLeuGluLysLysAlaLysAlaSer 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               46 pLeuArgGluAsnTyrGlyCysGluValValCysPheThrAlaAspValG 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       69 GCTGAAGGAACAA...GGCTATGACGTCATTGCCTATCTGGCCAACATTG 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30 ValValLeuAlaTyrSerGlyGlyLeuAspThrSerValIleValProTr 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19 GTGGTTCTGGCCTACAGTGGCGGCCTGGACACCTCGTGCATCCTCGTGTG 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Quality:
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alignment_block:
US-09-775-693-1 x US-09-708-427-79357
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                                                                                                                                                                                                            NAME/KEY: misc_feature

: LOCATION: 1..446

: OTHER INFORMATION: Ceres Seq. ID 1965188
US-09-708-427-79357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_documentation_block:
   Sequence 79357, Application US/09708427
   GENERAL INFORMATION:
   APPLICANT: N. ALEXANDROV et al.
                                                                     Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_name: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:US-09-708-427-79357
                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn version 3.1
SEQ ID NO 79357
LENGTH: 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID TITLE OF INVENTION: THEREBY FILE REFERENCE: 2750-1243P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature LOCATION: 1..446
OTHER INFORMATION: Xaa is any amino acid
                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Zea mays subsp. mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1163 CCACCGGGTTCATCAACATCAATTCCCTC 1191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1113 TGAGGAGCTGGTGAGCATGAACGTGCAGGGTGATTATGAGCCAACTGATG 1162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1063 AAGGGCCAGGTGTACATCCTCGGCCGGGAGTCCCCACTGTCTCTCTACAA 1112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         404 laGluGlyPheIleArgLeuTyrGlyLeu 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              387 gGluAspIleSerSerPheGluAsnGlyGluTleTyrAsnGlnAlaAspA 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     371 LysGlySerValAsnValAlaSerArgLysSerProTyrSerLeuTyrAr 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              354 etGluLysValThrAlaThrThrThrGlySerValThrLeuLysLeuTyr, 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    337 lTyralaGlyArgTrpPheAspProLeuArgGlnSerPheAspAlaPheM 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  963 GTATACCGGTTTACGGCCTAGCCCTGAGTGTGAATTTGTCCGCCACTGCA 1012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             321 GluThrMetGlnTrpLysAspIleIleAlaLeuLysTyrAlaGluLeuVa 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        913 GAAGTGCGCAAAATCAAACAAGGCCTGGGCTTGAAATTTGCTGAGCTGGT 962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      304 hrIleMetAlaAlaAlaValArgGluLeuGluSerLeuThrLeuAspArg 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 863 CCATCCTTTACCATGCTCATTTAGACATCGAGGCCTTCACCATGGACCGG 912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             287 nArgLeuValCysMetLysSerArgGlyValTyrGluThrProGlyGlyT 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     813 CCGCTTCATTGGAATGAAGTCCCGAGGTATCTACGAGACCCCCAGCAGCAGCA 862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 763 AACGAAGTCGCGGGCAAGCATGGCGTGGGCCGTATTGACATCGTGGAGAA 812
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                                                                                                                     Quality:
                                                                                                Ratio:
                                                                     866.50
2.947
74.809
                                                              Percent Identity: 45.547
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                                                                                                            Length:
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Align seg 1/1
       325
                                                863 CCATCCTTTACCATGCTCATTTAGACATCGAGGCCTTCACCATGGACCGG
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                                                                                                                                                                                                                                                                                                                                             713 TCAAGGATGGCACCACCACCAGACCTCCTTGGAGCTCTTCATGTACCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        151 ValAlaLysGluValGlyAlaAspAlaValAlaHisGlyCysThrGlyLy 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           313 ATCGCCCAGCGGGAGGGGGCCAAGTATGTGTCCCACGGCGCCCACAGGAAA 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     117 uTyrTleTyrProCysLeuArgAlaGlyAlaValTyrGluArgLysTyrL 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  213 GTTCATCTGGCCGGCCATCCAGTCCAGCGCACTGTATGAGGACCGCTACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         116 GCCAGAAGGAA...GACTTCGAGGAAGCCAGGAAGAAGGCACTGAAGCTT 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84
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                                                                                                                                                                                             hr {\tt IleMetAlaAlaAlaValArgGluLeuGluSerLeuThrLeuAspArg}
                                                                                              nArgLeuValCysMetLysSerArgGlyValTyrGluThrProGlyGlyT
                                                                                                                                                  CCGCTTCATTGGAATGAAGTCCCGAGGTATCTACGAGACCCCCAGCAGGCA 862
                                                                                                                                                                                                                                                AACGAAGTCGCGGGCAAGCATGGCGTGGGCCGTATTGACATCGTGGAGAA 812
                                                                                                                                                                                                                                                                                                                                                                                                uTyrLeuGluIleGlyIleIleAlaGlyValProValSerIle...AsnG 279
                                                                                                                                                                                                                                                                                                                                                                                                                                              CATTCTCGAGATCGAGTTCAAAAAAGGGGTCCCTGTGAAGGTGACCAACG 712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AspMetTyrMetMetSerIleAlaProGluAsnAlaProSerLysProGl 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGTCTCTACACGAAGACCCAGGACCCAGCCAAAGCCCCCAACACCCCTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCAGCTACGAGGCTGGAATCCTGGAGAACCCCAAGAACCAAGCGCCTCCA 612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               lProValSerLysLysSerIleTyrSerArgAspArgAsnLeuTrpHisL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCCGGTCACTCCCAAGAACCCCGTGGAGCATGGATGAGAACCTCATGCACA 562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ThrGlyArgGluAspAlaIleGluTyrAlaLysLysHisAsnValProVa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGATAAAGGTCATTGCTCCCTGGAGGATGCCTGAATTCTACAACCGGTTC 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGGGCCAAAAAGGTGTTCATTGAGGATGTCAGCAGGGAGTTTGTGGAGGA 212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCTGAAGGAACAA...GGCTATGACGTCATTGCCTATCTGGCCAACATTG 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ValValLeuAlaTyrSerGlyGlyLeuAspThrSerValIleValProTr 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           {\tt sGlyAsnAspGlnValArgPheGluLeuThrPheTyrAlaLeuAsnProG}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pLeuArgGluAsnTyrGlyCysGluValValCysPheThrAlaAspValG
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                                                   912
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seq_documentation_block:
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    Sequence 55743, Application US/09708427
    Sequence 55743, Application US/09708427
    TITLE OF INVERTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID TITLE OF INVERTION: THEREBY FILE REFERENCE: 2750-1243B
    CURRENT APPLICATION UNMBER: US/09/708,427
    CURRENT ENDING DATE: 2000-11-09
    NUMBER OF SEQ ID NOS: 85364
    SOFTWARE: PatentIn version 3.1
    SEQ ID NO 55743
    LENGTH: 426
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; LOCATION: 1..426
; OTHER INFORMATION: Ceres
US-09-708-427-55743
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          425 laGluGlyPheIleArgLeuTyrGlyLeu 434
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                                                                                                                                                                                                                           30 Val***LeuAlaTyrSerGlyGlyLeuAspThrSerValIleValProTr 46
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lyGlnGlyAlaIleGluLeuGluGlyLeuGluLysLysAlaLysAlaSer 79
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etGluLysValThrAlaThrThrGlySerValThrLeuLysLeuTyr 370
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alignment_block:
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; GENERAL INFORMATION:
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CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
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LOCATION: 1..447
OTHER INFORMATION: Ceres Seq.
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OTHER INFORMATION: Xaa
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euLeuGlyThrSerMetAlaArgProValIleAlaLysAlaMetValAsp
                  TCCTGGGCACCTCTCTTGCCAGGCCCTGCATCGCCCGCAAACAAGTGGAA 312
                                                                                                                                               GTTCATCTGGCCGGCCATCCAGTCCAGCGCACTGTATGAGGACCGCTACC 262
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1063 AAGGGCCAGGTGTACATCCTCGGCCGGGAGTCCCCCACTGTCTCTCTACAA 1112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             363 GGGGAACGATCAGGTCCGGTTTGAGCTCAGCTGCTACTCACTGGCCCCCC 412
                                                             1163 CCACCGGGTTCATCA 1177
                                                                                                                                                                                            1113 TGAGGAGCTGGTGAGCATGAACGTGCAGGGTGATTATGAGCCAACTGATG 1162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      247 AspMetTyrMetMetSerIleAlaProGluAsnAlaProSerLysProGl 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   613 GGTCTCTACACGAAGACCCAGGACCCAGCCAAAGCCCCCAACACCCCCTGA 662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  563 TCAGCTACGAGGCTGGAATCCTGGAGAACCCCAAGAACCAAGCGCCTCCA 612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                213 lProValSerLysLysSerIleTyrSerArgAspArgAsnLeuTrpHisL 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 513 CCCGGTCACTCCCAAGAACCCGTGGAGCATGGATGAGAACCTCATGCACA 562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         863 CCATCCTTTACCATGCTCATTTAGACATCGAGGCCTTCACCATGGACCGG 912
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                                                                                                                                                                                                                                                                                                                                                                                            375 etGluLysValThrAlaThrThrGlySerValThrLeuLysLeuTyr 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           358 lTyrAlaGlyArgTrpPheAspProLeuArgGlnSerPheAspAlaPheM 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            963 GTATACCGGTTTACGGCCTAGCCCTGAGTGTGAATTTGTCCGCCACTGCA 1012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      913 GAAGTGCGCAAAATCAAACAAGGCCTGGGCTTGAAATTTGCTGAGCTGGT 962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        325 hrIleMetAlaAlaAlaValArgGluLeuGluSerLeuThrLeuAspArg 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    763 AACGAAGTCGCGGCAAGCATGGCGTGGGCCGTATTGACATCGTGGAGAA 812
425 ProArgGlySerSer 429
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                                                                                                                              gGluAspIleSerSerPheGluAsnGlyGluIleTyr.AsnGln***Thr 424
                                                                                                                                                                                                                                                          LysGlySerValAsnValAlaSerArgLysSerProTyrSerLeuTyrAr 408
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seq_name: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:US-09-897-516-5764

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seq_documentation_block:
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US-09-897-516-5764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_block: us-09-897-516-5764
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 5764, Application US/09897516 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to: US-09-897-516-5764 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 5764
LENGTH: 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hueslay, Joseph E.
APPLICANT: Krasomil-Osterfeld, Karina C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Corbin, David R. APPLICANT: Goldman, Barry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/215, 161
PRIOR FILING DATE: 2000-06-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/897,516
CURRENT FILING DATE: 2001-06-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Xenorhabdus sp. Genome FILE REFERENCE: 38-21(51847)B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Slater, Steven C. APPLICANT: Spiridonov, Sergei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 8409
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                                                                                                                                                         131 yLysGlyAsnAspGlnValArgPheGluSerThrTyrThrAlaLeuAlaP 148
                                                                                                                                                                                                                                                                   115 GluLeuAlaLeuLysValGlyAlaAspAlaLeuAlaHisGlyAlaThrGl 131
                                                                                                                                                                                                                                                                                                                     310 GAAATCGCCCAGCGGGAGGGGGCCAAGTATGTGTCCCACGGCGCCCACAGG 359
                                                                                                                                                                                                                                                                                                                                                                                                                            260 ACCTCCTGGGCACCTCTTGCCAGGCCCTGCATCGCCCGCAAACAAGTG 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       210 GGAGTTCATCTGGCCGGCCATCCAGTCCAGCGCACTGTATGAGGACCGCT 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               113 TTGGCCAG...AAGGAAGACTTCGAGGAAGCCAGGAAGAAGAAGCCACTGAAG
460 TTCAAGGGCCGCAATGACCTGATGGAGTACGCAAAGCAACACGGGATTCC 509
                                                                                                                                                                                                                 360 AAAGGGGAACGATCAGGTCCGGTTTGAGCTCAGCTGCTACTCACTGGCCC 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              160 CTTGGGGCCAAAAAGGTGTTCATTGAGGATGTCAGCAGGGAGTTTGTGGA 209
                                                                                                          410 CCCAGATAAAGGTCATTGCTCCCTGGAGGATGCCTGAATTCTACAACCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ## 31 SGluTyrValTyrProValLeuLysThrGlyAlabeuTyrGluGlySerT 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      65 SerGlyAlaSerGluCysHisIleAlaAspLeuArgGluGluPheIleLy 81
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                                                                                                                                                                                                                                                                                                                                                                                98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19 GTGGTTCTGGCCTACAGTGGCGGCCTGGACACCTCGTGCATCCTCGTGTG
                                                                                                                                                                                                                                                                                                                                                                          yrLeuLeuGlyThrSerMetAlaArgProIleIleAlaLysAlaGlnVal 114
                                                          roHisLeuLysValValAlaProTrpArgGluTrpAsp......
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2.836
71.358
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seq_documentation_block:
    sequence 11258, Application US/09708427
    GENERAL INFORMATION:
    APPLICANT: N. ALEXANDROV et al.
    TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
    TITLE OF INVENTION: THEREBY
    TITLE OF INVENTION: THEREBY
    TITLE OF INVENTION: THEREBY
                                                                                                                                                                                                                                                                                 seq_name: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:US-09-708-427-11258
CURRENT APPLICATION NUMBER: US/09/708,427
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             960 GGTGTATACCGGTTTACGGCCTAGCCCTGAGTGTGAATTTGTCCGCCACT 1009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    810 GAACCGCTTCATTGGAATGAAGTCCCGAGGTATCTACGAGACCCCAGCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              510 CATCCCGGTCACTCCCAAGAACCCGTGGAGCATGGATGAGAACCTCATGC 559
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 isAlaGluGlyPheIleArgLeuHisSerLeuSer...SerArgIleArg 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATGCCACCGGGTTCATCAACATCAATTCCCTCAGGCTGAAGGAATATCAT 1209
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alignment_block:
US-09-775-693-1 x US-09-708-427-11258
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; LOCATION: 1..498
; OTHER INFORMATION: Ceres Seq. ID 1822815
US-09-708-427-11258
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 11258
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Arabidopsis thaliana
FEATURE:
NAME/RBY: misc_feature
LOCATION: 1. 498
OTHER INFORMATION: Xaa is any amino acid
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TYPE: PRT
                                                                                                                                                                                                                                                                 236 luLeuLysValValAlaProTrpArgGluTrpGlu......Ile
                     563 TCAGCTACGAGGCTGGAATCCTGGAGAACCCCAAGAACCAAGCGCCTCCA 612
                                                                  265 lProValThrLysLysSerIleTyrSerArgAspArgAsnLeuTrpHisL 282
                                                                                                                    513 CCCGGTCACTCCCAAGAACCCGTGGAGCATGGATGAGAACCTCATGCACA 562
                                                                                                                                                                    249 GlnGlyArgGluAspAlaIleGluTyrAlaLysLysHisAsnValProVa 265
                                                                                                                                                                                                                         463 AAGGGCCGCAATGACCTGATGGAGTACGCAAAGCAACACGGGATTCCCAT 512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             313 ATCGCCCAGCGGGAGGGGGCCAAGTATGTGTCCCACGGCGCCCACAGGAAA 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            194 pPheIlePheProCysLeuArgAlaGlyAlaIleTyrGluArgLysTyrL 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          263 TCCTGGGCACCTCTTTGCCAGGCCCTGCATCGCCCGCAAACAAGTGGAA 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            213 GTTCATCTGGCCGGCCATCCAGTCCAGCGCACTGTATGAGGACCGCTACC :||||||:::|||||:::|||||| :::|||||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 178 GlyAlaSerGlnLeuValValLysAspLeuThrGluGluPheValLysAs 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 163 GGGGCCAAAAAGGTGTTCATTGAGGATGTCAGCAGGGAGTTTGTGGAGGA 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   161 lyGlnGlyIleLysGluLeuGluGlyLeuGluGlnLysAlaLysAlaSer 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     116 GCCAGAAG...GAAGACTTCGAGGAAGCCAGGAAGAAGCACTGAAGCTT 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  144 pLeuLysGluAsnTyrGlyCysGluValValCysPheThrAlaAspValG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     128 ValValLeuAlaTyrSerGlyGlyLeuAspThrSerValIleValProTr 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19 GTGGTTCTGGCCTACAGTGGCGGCCTGGACACCTCGTGCATCCTCGTGTG 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69 GCTGAAGGAACAA...GGCTATGACGTCATTGCCTATCTGGCCAACATTG 115
                                                                                                                                                                                                                                                                                                                        AGATAAAGGTCATTGCTCCCTGGAGGATGCCTGAATTCTACAACCGGTTC 462
                                                                                                                                                                                                                                                                                                                                                                              .....ValArgPheGluLeuThrPhePheSerLeuAsnProG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             euLeuGlyThrSerMetAlaArgProValIleAlaLys...... 223
GGGGAACGATCAGGTCCGGTTTGAGCTCAGCTGCTACTCACTGGCCCCCC 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    498
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ratio:
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2.890
71.212
2000-11-09
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42.172
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seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 12974, Application US/09675784A GENERAL INFORMATION:
SEQ ID NO 12974
LENGTH: 257
                                                                                                                                                                                    APPLICANT: GREENE, JONATHAN R.
TITLE OF INVENTION: ASPERGILLUS FUNIGATUS NUCLEIC ACIDS AND POLYPEPTIDES.
TITLE OF INVENTION: AND USES THEREFOR
FILE REFERENCE: 2976-4020US1
                                                                                                                              CURRENT APPLICATION NUMBER: US/09/675,784A
CURRENT FILING DATE: 2000-09-29
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                                                  PRIOR APPLICATION NUMBER: 60/156,338 PRIOR FILING DATE: 1999-09-29 NUMBER OF SEQ ID NOS: 13925
                                                                                                                                                                                                                                                                                               APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1063 AAGGGCCAGGTGTACATCCTCGGCCGGGAGTCCCCACTGTCTCTCTACAA 1112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            713 TCAAGGATGGCACCACCCACCAGACCTCCTTGGAGCTCTTCATGTACCTG 762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    663 CATTCTCGAGATCGAGTTCAAAAAAGGGGTCCCTGTGAAGGTGACCAACG 712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       299 AspMetTyrMetMetSerValAspProGluAspAlaProAspGlnProGl 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            613 GGTCTCTACACGAAGACCCAGGACCCAAGCCCAAAGCCCCCCAACACCCCCTGA 662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  282 euSerHisGluGlyAspLeuLeuGluAspProAlaAsnGluProLysLys 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1163 CCACCGGGTTCATCAACATCAATTCCCTCAGGCTGAAG 1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        813 CCGCTTCATTGGAATGAAGTCCCGAGGTATCTACGAGACCCCCAGCAGGCA 862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                {\tt 344~AsnThrIleGlyGlyLysHisGlyIleGlyArgIleAspMetValGluAs}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               763 AACGAAGTCGCGGGCAAGCATGGCGTGGGGCCGTATTGACATCGTGGAGAA 812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    315 uTyrIleGluIleGlyIleGluSerGlyLeuProValAlaLeuAsnGly. 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     863 CCATCCTTTACCATGCTCATTTAGACATCGAGGCCTTCACCATGGACCGG 912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 427 etGluLysIleThrGluThrThrThrGlySerValThrLeuLysLeuTyr 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               410 lTyrAlaGlyArgTrpPheAspProLeuArgGluSerMetAspAlaPheM 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       963 GTATACCGGTTTACGGCCTAGCCCTGAGTGTGAATTTGTCCGCCACTGCA 1012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          394 GluSerIleGlnValLysAspThrLeuAlaLeuLysTyrAlaGluMetVa 410
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  377 hrIleLeuPheAlaAlaValGlnGluLeuGluSerLeuThrLeuAspArg 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        460 gGlnAspIleSerSerPheGluGlySerGluIleTyrAsnGlnAlaAspA 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   477 laAlaGlyPheIleArgLeuTyrGlyLeuProMetLys 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .....LysalaLeuSerProAlaThrLeuLeuAlaGluLeu 343
                                                                                                                                                                                                                                                                                       KESSLER, MARCO
NOLLING, JORK
ZENG, QIANDONG
                                                                                                                                                                                                                                                                                                                                                                              SHIMER JR., GEORGE H.
                                                                                                                                                                                                                                                                                                                                                                                                        SHAW, KAREN J
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; ORGANISM: Aspergillus fumigatus US-09-675-784A-12974
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
seq_name: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:US-09-708-427-79359
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    122 IleAspValAlaLysArgGluGlyCysPheAlaValSerHisGlyCysTh 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       257 GCTACCTCCTGGGCACCTCTTGCCAGGCCCTGCATCGCCCGCAAACAA 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             207 GGAGGAGTTCATCTGGCCGGCCATCCAGTCCAGCGCACTGTATGAGGACC 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      157 AAGCTTGGGGCCAAAAAGGTGTTCATTGAGGATGTCAGCAGGGAGTTTGT 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          407 CCCCCCAGATAAAGGTCATTGCTCCCTGGAGGATGCCTGAATTCTACAAC 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                138 rGlyLysGlyAsnAspGlnValArgPheGluLeuAlaPheTyrAlaLeuG 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     357 AGGAAAGGGGAACGATCAGGTCCGGTTTGAGCTCAGCTGCTACTCACTGG 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 307 GTGGAAATCGCCCAGCGGGAGGGGGCCAAGTATGTGTCCCACGGCGCCCAC 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               457 CGGTTCAAGGGCCGCAATGACCTGATGGAGTACGCAAAGCAACACGGGAT 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                657 CCCTGACATTCTCGAGATCGAGTTCAAAAAAGGGGTCCCTGTGAAGGTG 705
                                                                                                                                  557 TGCACATCAGCTACGAGGCTGGAATCCTGGAGAACCCCAAGAACCAAGCG 606
                                                                                                                                                                                                                                                                                                               188 eProValThrSerThrLysAlaLysProTrpSerMetAspGluAsnLeuA 205
                                                                                                                                                                                                                                                                                                                                                         507 TCCCATCCCGGTCACTCCCAAGAACCCGTGGAGCATGGATGAGAACCTCA 556
                                                                                                                                                                                                                                                                                                                                                                                                   172 ArgPheAlaGlyArgAsnAspLeuLeuSerTyrAlaAlaGluLysGlyIl 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   88 eGluGlnLeuCysPheProAlaIleAlaCysAsnAlaIleTyrGluAsnV 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       72 LysLeuGlyAlaValLysCysGluIleAlaAspLeuArgArgGluPheIl 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22 SerLysGlyLysValCysLeuAlaPheSerGlyGlyLeuAspThrSerVa 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 AGCAAAGGCTCCGTGGTTCTGGCCTACAGTGGCGGCCTGGACACCTCGTG 56
                                                 nProGluAspPheThrValHisPheGluThrGlyIleProValLysLeu 254
                                                                                                                                                                               CCTCCAGGTCTCTACACGAAGACCCAGGACCCAGCCAAAGCCCCCAACAC 656
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4.059
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alignment_block:
US-09-775-693-1 x US-09-708-427-79359
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Ratio: 2.953
Percent Similarity: 72.787
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CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: PatentIn version 3.1
SEQ ID NO 79359
LENGTH: 308
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TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES

TITLE OF INVENTION: THEREBY

FILE REFERENCE: 2750-1243P
144 .....LeuSerProAlaSerLeuLeuAlaGluLeuAsnGluIleGlyGl 158
                                                  727 ACCCACCAGACCTCCTTGGAGCTCTTCATGTACCTGAACGAAGTCGCGGG 776
                                                                                                          130 lyIleIleAlaGlyValProValSerIle...AsnGlyArgAsp..... 143
                                                                                                                                                               677 AGTTCAAAAAAGGGGTCCCTGTGAAGGTGACCAACGTCAAGGATGGCACC 726
                                                                                                                                                                                                                       113 tSerIleAlaProGluAsnAlaProSerLysProGluTyrLeuGluIleG 130
                                                                                                                                                                                                                                                                            627 GACCCAGGACCCAGCCAAAGCCCCCAACACCCCTGACATTCTCGAGATCG 676
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OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
LOCATION: 1..308
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ORGANISM: Zea mays subsp. mays
                                                                                                                                                                                                                                                                                                                                                                                            577 GGAATCCTGGAGAACCCCAAGAACCAAGCGCCTCCAGGTCTCTACACGAA 626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      527 AGAACCCGTGGAGCATGGATGAGAACCTCATGCACATCAGCTACGAGGCT 576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               477 CCTGATGGAGTACGCAAAGCAACACGGGATTCCCATCCCGGTCACTCCCA 526
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      377 TCCGGTTTGAGCTCAGCTGCTACTCACTGGCCCCCCAGATAAAGGTCATT 426
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                                                                                                                                                                                                                                                                                                                                    97 AspIleLeuGluAspProAlaAsnGluProLysGluAspMetTyrMetMe 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           327 GGGGGCCAAGTATGTGTCCCACGGCGCCACAGGAAAGGGGAACGATCAGG 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     277 CTTGCCAGGCCCTGCATCGCCCGCAAACAAGTGGAAATCGCCCAGCGGGA 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                 80 ysSerIleTyrSerArgAspArgAsnLeuTrpHisLeuSerHisGluGly 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63 pAlaIleGluTyrAlaLysLysHisAsnValProValProValSerLysL 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51 AlaProTrpArgGluTrpAsp......IleThrGlyArgGluAs 63
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alignment_block:
US-09-775-693-1 x US-09-708-427-55744
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                                                                             Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: Patentin version 3.1
SEQ ID NO 5574
LENGTH: 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 55744, Appl
GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID FILE REFERENCE: 2750-1243P
                                                                                                                                                                                                                                  NAME/KEY: misc_feature
LOCATION: 1..309
OTHER INFORMATION: Ceres Seq. ID 1935963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: N. ALEXANDROV et al
                                                                                                                                                                                                                                                                                                          NAME/KEY: misc_feature
LOCATION: 1..309
OTHER INFORMATION: Xaa is any amino acid
                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Zea mays subsp. mays
                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1177 AACATCAATTCCCTC 1191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1127 GCATGAACGTGCAGGGTGATTATGAGCCAACTGATGCCACCGGGTTCATC 1176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1077 CATCCTCGGCCGGGAGTCCCCCACTGTCTCTACAATGAGGAGCTGGTGA 1126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1027 GAGCGAGTGGAAGGGAAAGTGCAGGTGTCCGTCCTCAAGGGCCAGGTGTA 1076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        292 ArgLeuTyrGlyLeu 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        275 erPheGluAsnGlyGluIleTyrAsnGlnAlaAspAlaGluGlyPheIle 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    258 nValAlaSerArgLysSerProTyrSerLeuTyrArgGluAspIleSerS 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                242 AlaThrThrGlySerValThrLeuLysLeuTyrLysGlySerValAs 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         977 GCCCTAGCCCTGAGTGTGAATTTGTCCGCCACTGCATCGCCAAGTCCCAG 1026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            225 rpPheAspProLeuArgGlnSerPheAspAlaPheMetGluLysValThr 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        927 CAAACAAGGCCTGGGCTTGAAATTTGCTGAGCTGGTGTATACCGGTTTAC 976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 192 AlaValArgGluLeuGluSerLeuThrLeuAspArgGluThrMetGlnTr 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              877 GCTCATTTAGACATCGAGGCCTTCACCATGGACCGGGAAGTGCGCAAAAT 926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           175 etLysSerArgGlyValTyrGluThrProGlyGlyThrIleMetAlaAla 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          827 TGAAGTCCCGAGGTATCTACGAGACCCCAGCAGGCACCATCCTTTACCAT 876
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                                                                                                                            Quality:
                                                                                                      Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Application US/09708427
                                                                        639.50
2.947
72.093
                                                                     Percent Identity: 44.850
                                                                                                                       Length:
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Align seg 1/1 to: US-09-708-427-55744 from: 1

to: 309

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1027
1127 GCATGAACGTGCAGGGTGATTATGAGCCAACTGATGCCACCGGGTTCATC 1176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        277 CTTGCCAGGCCCTGCATCGCCCGCAAACAAGTGGAAATCGCCCAGCGGGA 326
                                                          258 nValAlaSerArgLysSerProTyrSerLeuTyrArgGluAspIleSerS
                                                                                                                                                                                 242 AlaThrThrGlySerValThrLeuLysLeuTyrLysGlySerValAs 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        130 lyIleIleAlaGlyValProValSerIle...AsnGlyArgAsp..... 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |||||||
| 17 ||GlyAlaAspAlaValAlaHisGlyCysThrGlyLysGlyAsnAspGlnV 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MetAlaArgProValIleAlaLysAlaMetValAspValAlaLysGluVa 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCTGATGGAGTACGCAAAGCAACACGGGATTCCCATCCCGGTCACTCCCA 526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCTCCCTGGAGGATGCCTGAATTCTACAACCGGTTCAAGGGCCGCAATGA 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCCGGTTTGAGCTCAGCTGCTACTCACTGGCCCCCCAGATAAAGGTCATT 426
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                                                                                                                    CATCCTCGGCCGGGAGTCCCCACTGTCTCTCTACAATGAGGAGCTGGTGA 1126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGAAGTCCCGAGGTATCTACGAGACCCCAGCAGCAGCACCCATCCTTTACCAT 876
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGAACCCGTGGAGCATGGATGAGAACCTCATGCACATCAGCTACGAGGCT 576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pAlaIleGluTyrAlaLysLysHisAsnValProValProValSerLysL 80
                                                                                                                                                                                                                                              GAGCGAGTGGAAGGGAAAGTGCAGGTGTCCGTCCTCAAGGGCCAGGTGTA 1076
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGTTCAAAAAAGGGGTCCCTGTGAAGGTGACCAACGTCAAGGATGGCACC 726
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                                                                                                                                                                                                                                                                                                            rpPheAspProLeuArgGlnSerPheAspAlaPheMetGluLysValThr 241
                                                                                                                                                                                                                                                                                                                                                                      GGCCTAGCCCTGAGTGTGAATTTGTCCGCCACTGCATCGCCAAGTCCCAG 1026
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erPheGluAsnGlyGluIleTyr.AsnGln***ThrProArgGlySerSe

291

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NAME/KEY: misc_feature
LCCATION: 1..283
COTHER INFORMATION: Ceres Seq.
US-09-708-427-11259
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US-09-775-693-1 x US-09-708-427-11259
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1 to: US-09-708-427-11259 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: PatentIn version 3.1
SEQ ID NO 11259
LENGTH: 283
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Xaa is any amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature LOCATION: 1..283
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1177 A 1177
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                                                                                                                                       577 GGAATCCTGGAGAACCCCAAGAACCAAGCGCCTCCAGGTCTCTACACGAA 620
                                                                                                                                                                                                                                     527 AGAACCCGTGGAGCATGGATGAGAACCTCATGCACATCAGCTACGAGGCT 576
                                                                                                                                                                                                                                                                                                                              477 CCTGATGGAGTACGCAAAGCAACACGGGATTCCCATCCCGGTCACTCCCA 526
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                                                                                                                                                                                                                                                                               38 pAlaIleGluTyrAlaLysLysHisAsnValProValProValThrLysL
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tSerValAspProGluAspAlaProAspGlnProGluTyrIleGluIleG 105
                                            GACCCAGGACCCAGCCAAAGCCCCCAACACCCCTGACATTCTCGAGATCG 676
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AspLeuLeuGluAspProAlaAsnGluProLysLysAspMetTyrMetMe 88
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Ratio:
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2.875
67.532
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seq_documentation_block:

Sequence 32991, Application US/10029386

GENERAL INFORMATION:

APPLICANT: Penn, Sharron G.

APPLICANT: Rank, David R.

APPLICANT: Hanzel, David R.

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR FILE REFERENCE: AEDMICA-X-2
; OTHER INFORMATION:
; OTHER INFORMATION:
US-10-029-386-32991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_name: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep:US-10-029-386-32991
                                                                                                                                                                                                                                                                                                                              SEQ ID NO 32991
LENGTH: 138
                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
                    OTHER INFORMATION: MAP TO AC004616.1
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.83
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.1
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.7
OTHER INFORMATION: SWISSPROT HIT: P00966, EVALUE 6.00e-48
                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens
                                                                                                                                                                                                                                    FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1177 AACATCAATTCCCTCAGGCTGAAG 1200
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:|||:::||||||:::||||||:::|||||||:::|||
183 ltysaspThrLeuAlaLeuLysTyrAlaGluMetValTyrAlaGlyArgT 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  105 lyIleGluSerGlyLeuProValAlaLeuAsnGly......... 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ArgLeuTyrGlyLeuProMetLys 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCATGAACGTGCAGGGTGATTATGAGCCAACTGATGCCACCGGGTTCATC
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                                                                                                                                                                                                                                                                                                         PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    250
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alignment_block:
US-09-775-693-1 x US-10-029-386-32991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Quality: 477.00
Ratio: 4.500
Percent Similarity: 96.364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to: US-10-029-386-32991 from: 1
                 301 AAACAAGTGGAAAATCGCCCAGCGGGAGGGG 330
                                                                     101 ATCTGGCCAACATTGGCCAGAAGGAAGACTTCGAGGAAGCCAGGAAGAAG
                                                                                                                                                                                                                                             151 GCACTGAAGCTTGGGGCCAAAAAGGTGTTCATTGAGGATGTCAGCAGGGA 200
                                                                                                                                                                                                                                 78
                                                                                                                                                                                                                                                                                                    61 yrLeuAlaLysIleSerGlnLysGluAspPheGluAspAspArgLysLys
                                                                                                                                                                                                                                                                                                                                                                                                51 CTCGTGCATCCTCGTGTGGGCTGAAGGAACAAGGCTATGACGTCATTGCCT 100
                                                                                                                                                                                                                                                                                                                                                                                44 rSerCysIleLeuMetTrpLeuLysGluGlnGlyHisAspValIleAlaT
                                                                                                                                                                                                                                                                                                                                                                                                                                                        28 ValSerSerLysGlySerMetValLeuAlaHisSerGlyGlyLeuAspTh 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ATGTCCAGCAAAGGCTCCGTGGTTCTGGCCTACAGTGGCGGCCTGGACAC
LysGlnValGluIleThrGlnGlnGluGly 137
                                                                                                         AGGACCGCTACCTCCTGGGCACCTCTCTTGCCAGGCCCTGCATCGCCCGC 300
                                                                                                                                                                                                                           AlaTrpLysLeuGlyAlaLysLysValPheIleAspAspValSerArgAs
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Gaps: 0
Percent Identity: 84.545
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